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http://www.cas.org/ONLINE/UG/regprops.html

L1 4 S DLMGYIPAV/SQSP

L1 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN

RN 827608-26-4 REGISTRY

CN L-Leucine, L-α-aspartyl-L-leucyl-L-methionylglycyl-L-tyrosyl-L-isoleucyl-L-prolyl-L-alanyl-L-valylglycyl-L-alanyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 4: PN: WO2005004910 PAGE: 51 claimed sequence

SQL 13

SEQ 1 DLMGYIPAVG APL

=======

HITS AT: 1-9

REFERENCE 1: 142:154229

L1 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN

RN 260232-79-9 REGISTRY

CN Hepatitis C core antigen [139-alanine] (hepatitis C virus) (9CI) (CA INDEX NAME)

OTHER NAMES:

1

1: PN: WO0011186 SEQID: 2 claimed protein CN CI MAN SQL 191 1 MSTNPKPOKK NKRNTNRRPO DVKFPGGGQI VGGVYLLPRR GPRLGVRATR SEO 51 KTSERSOPRG RROPIPKARR PEGRTWAQPG YPWPLYGNEG CGWAGWLLSP 101 RGSRPSWGPT DPRRRSRNLG KVIDTLTCGF ADLMGYIPAV GAPLGGAARA 151 LAHGVRVLED GVNYATGNLP GCSFSIFLLA LLSCLTVPAS A 132-140 HITS AT: REFERENCE 1: 132:206926 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN L1215295-45-7 REGISTRY RN $L-Valine, \ L-\alpha-aspartyl-L-leucyl-L-methionylglycyl-L-tyrosyl-L-methionylglycyl-L-me$ isoleucyl-L-prolyl-L-alanyl- (9CI) (CA INDEX NAME) OTHER NAMES: 12: PN: WO2004084938 PAGE: 27 claimed sequence 1: PN: WO0011186 SEQID: 1 claimed protein 48: PN: WO2005004910 PAGE: 52 claimed sequence SQL 9 1 DLMGYIPAV SEQ ======= HITS AT: 1-9 143:373377 REFERENCE 1: 142:154229 REFERENCE 2: REFERENCE 3: 141:409214 REFERENCE 141:330768 134:285564 REFERENCE 5: REFERENCE 6: 132:206926 REFERENCE 7: 129:329617 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN L1RN 199533-14-7 REGISTRY L-Valine, L-alanyl-L-α-aspartyl-L-leucyl-L-methionylglycyl-L-CN tyrosyl-L-isoleucyl-L-prolyl-L-alanyl- (9CI) (CA INDEX NAME) SQL 10 SEO 1 ADLMGYIPAV ======= HITS AT: 2-10 REFERENCE 1: 128:33617 FILE 'CAPLUS' ENTERED AT 16:48:58 ON 24 JAN 2006 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

Searcher : Shears 571-272-2528

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L2 8 L1

L2 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 14 Oct 2005

ACCESSION NUMBER: 2005:1103622 CAPLUS

DOCUMENT NUMBER: 143:373377

TITLE: Method for solubilizing peptide mixtures INVENTOR(S): Zauner, Wolfgang; Kritsch, Constantia;

Heinrich-Cseh, Christa; Berger, Agnes

. Intercell AC Austria

PATENT ASSIGNEE(S): Intercell AG, Austria SOURCE: PCT Int. Appl., 21 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PAT	PATENT NO.						KIND DATE			APPL:	DATE					
WO	2005094891								Ī	70 2	005-		20050311			
	W:	ΑE,	AG,	AL,	AM,	AT,	ΑU,	ΑZ,	BA,	BB,	BG,	BR,	BW,	BY,	ΒZ,	CA,
		CH,	CN,	CO,	CR,	CU,	CZ,	DE,	DK,	DM,	DZ,	EC,	EE,	EG,	ES,	FI,
		GB,	GD,	GE,	GH,	GM,	HR,	HU,	ID,	IL,	IN,	IS,	JP,	ΚE,	KG,	KP,
		KR,	ΚZ,	LC,	LK,	LR,	LS,	LT,	LU,	LV,	MA,	MD,	MG,	MK,	MN,	MW,
		MX,	MZ,	NA,	NI,	NO,	ΝZ,	OM,	PG,	PH,	PL,	PT,	RO,	RU,	SC,	SD,
		SE,	SG,	SK,	SL,	SM,	SY,	ТJ,	TM,	TN,	TR,	TT,	TZ,	UA,	UG,	US,
		UΖ,	VC,	VN,	YU,	ZA,	ZM,	zw								
	RW:	BW,	GH,	GM,	KE,	LS,	MW,	MZ,	NA,	SD,	SL,	SZ,	TZ,	UG,	ZM,	ZW,
		AM,	ΑZ,	BY,	KG,	ΚZ,	MD,	RU,	ТJ,	TM,	ΑT,	ΒE,	BG,	CH,	CY,	CZ,
		DE,	DK,	EE,	ES,	FI,	FR,	GB,	GR,	HU,	ΙE,	IS,	IT,	LT,	LU,	MC,
		NL,	PL,	PT,	RO,	SE,	SI,	SK,	TR,	BF,	ВJ,	CF,	CG,	CI,	CM,	GA,
		GN,	GQ,	GW,	ML,	MR,	ΝE,	SN,	TD,	TG						
PRIORITY	APP	LN.	INFO	.:						EP 2	004-	A 20040312				

AB Described is a method for making a pharmaceutical preparation comprising the solubilization of a peptide mixture, characterized in that the peptide mixture is solubilized by an aqueous solution containing at least one organic

acid selected from the group consisting of formic acid, acetic acid, propionic acid, butyric acid and halogenated or hydroxylated forms thereof.

IT 215295-45-7 RL: PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (method for solubilizing peptide mixts.) ANSWER 2 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN L2Entered STN: 20 Jan 2005 ACCESSION NUMBER: 2005:55094 CAPLUS 142:154229 DOCUMENT NUMBER: Hepatitis C virus vaccines comprise HLA-A2, -DR1 TITLE: and -DR7 epitopes and immune adjuvant Buschle, Michael; Frisch, Juergen; Klade, INVENTOR(S): Christoph; Lingnau, Karen; Zauner, Wolfgang; Zettlmeissl, Gerd Intercell AG, Austria PATENT ASSIGNEE(S): PCT Int. Appl., 59 pp. SOURCE: CODEN: PIXXD2 DOCUMENT TYPE: Patent English LANGUAGE: FAMILY ACC. NUM. COUNT: 7 PATENT INFORMATION: APPLICATION NO. DATE PATENT NO. KIND DATE _____ _____ ____ WO 2004-EP7540 20040709 WO 2005004910 A2 20050120 A3 20050421 WO 2005004910 AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG EP 2003-450171 PRIORITY APPLN. INFO.: A 20030711 EP 2004-450062 A 20040312 MARPAT 142:154229 OTHER SOURCE(S): Disclosed is a Hepatitis C virus (HCV) vaccine comprising at least two epitopes, each from a different hotspot epitope, wherein a hotspot epitope is defined as an epitope containing peptide selected from the group consisting of KFPGGGQIVGGVYLLPRRGPRLGVRATRK, GYKVLVLNPSVAAT, AYAAQGYKVLVLNPSVAAT, DLMGYIP(A/L)VGAPL, GEVQVVSTATQSFLATCINGVCWTV, HMWNFISGIQYLAGLSTLPGNPA, VDYPYRLWHYPCT(V/I)N(F/Y)TIFK(V/I)RMYVGGVEHRL, AAWYELTPAETTVRLR, GQGWRLLAPITAYSQQTRGLLGCIV, IGLGKVLVDILAGYGAGVAGALVAFK, FTDNSSPPAVPQTFQV, LEDRDRSELSPLLLSTTEW, YLVAYOATVCARAQAPPPSWD, MSTNPKPQRKTKRNTNR, LINTNGSWHINRTALNCNDSL, TTILGIGTVLDQAET, FDS(S/V)VLCECYDAG(A/C)AWYE, ARLIVFPDLGVRVCEKMALY,

and TTLLFNILGGWVAAQ.
IT 215295-45-7 827608-26-4

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

Searcher : Shears 571-272-2528

AFCSAMYVGDLCGSV, GVLFGLAYFSMVGNW, VVCCSMSYTWTGALITPC, TRVPYFVRAQGLIRA

(HCV vaccines comprise HLA-A2, -DR1 and -DR7 epitopes and immune adjuvant)

L2 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 07 Oct 2004

ACCESSION NUMBER: 2004:817738 CAPLUS

DOCUMENT NUMBER:

TITLE: Vaccines comprising antigen, polycationic peptide

and immunostimulatory deoxynucleic acid against

viral infection

141:330768

INVENTOR(S):
Buschle, Michael; Habel, Andre; Fritz, Joerg;

Prinz, Karin; Lingnau, Karen

PATENT ASSIGNEE(S):

Intercell A.-G., Austria PCT Int. Appl., 62 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

SOURCE:

LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PA'	PATENT NO.						DATE			APPL	ICAT		DATE			
WO	WO 2004084938						2004	1007	1	WO 2	004-		20040322			
	W:	•	•				AU,	•	-	-	-	-	-			
		CH,	CN,	CO,	CR,	CU,	CZ,	DE,	DK,	DM,	DZ,	EC,	EE,	EG,	ES,	FI,
		GB,	GD,	GE,	GH,	GM,	HR,	HU,	ID,	IL,	IN,	IS,	JP,	KE,	KG,	KP,
		KR,	ΚZ,	LC,	LK,	LR,	LS,	LT,	LU,	LV,	MA,	MD,	MG,	MK,	MN,	MW,
		MX,	MZ,	NA,	NI,	NO,	NZ,	OM,	PG,	PH,	PL,	PT,	RO,	RU,	SC,	SD,
		SE,	SG,	SK,	SL,	SY,	ТJ,	TM,	TN,	TR,	TT,	TZ,	UA,	UG,	US,	UZ,
		VC,	VN,	YU,	ZA,	ZM,	zw									
	RW:	BW,	GH,	GM,	KE,	LS,	MW,	MZ,	SD,	SL,	SZ,	TZ,	UG,	ZM,	ZW,	AM,
		•	•	•	•		RU,	-		•	-	-	-	-		
							GB,									
		RO,	SE,	SI,	SK,	TR,	BF,	ΒJ,	CF,	CG,	CI,	CM,	GΑ,	GN,	GQ,	GW,
			MR,													
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EP																0040322
	R:						ES,									
		•	•	SI,	LT,	LV,	FI,	RO,	MK,	CY,	AL,	TR,	BG,	CZ,	EE,	HU,
		PL,													_	
PRIORIT	RIORITY APPLN. INFO.:									EP 2	003-	4500	72		A 2	0030324
										EP 2	003-	4500	84	;	A 2	0030411
										EP 2	003-	4501	71	į	A 2	0030711
										WO 2	004-	EP30	02	,	₩ 2	0040322

- AB The invention refers to an improved vaccine against infections with pathogens, especially viral pathogens, comprising an antigen, a peptide of the formula R1-XZXZN-XZX-R2 and an immunostimulatory deoxynucleic acid containing deoxyinosine and/or deoxyuridine residues. Prepared were influenza vaccine compns. and hepatitis B vaccine compns.
- IT 215295-45-7

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(vaccines comprising antigen, polycationic peptide and

immunostimulatory deoxynucleic acid against viral infection)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR

THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 19 Apr 2004

ACCESSION NUMBER: 2004:313986 CAPLUS

DOCUMENT NUMBER: 141:409214

TITLE: Detection of serum heat shock protein 70 level in

patients with hepatitis C infection and its role in cytotoxicity of CTLs induced by HSP70-HCV

peptide complex

AUTHOR(S): Men, Ke; Wang, Xia; Xu, Dezhong; Zhou, Hongchao;

Zhang, Jingxia

CORPORATE SOURCE: Division of Preventive Medicine, Fourth Military

Medical University, Xian, Shanxi Province, 710032,

Peop. Rep. China

SOURCE: Xibao Yu Fenzi Mianyixue Zazhi (2003), 19(3),

305-307

CODEN: XFMZFM; ISSN: 1007-8738

PUBLISHER: Xibao Yu Fenzi Mianyixue Zazhi Bianjibu

DOCUMENT TYPE: Journal LANGUAGE: Chinese

The serum HSP70 in patients with hepatitis C was detected and its role in cytotoxicity of specific CTLs induced by HSP70-HCV peptide complex was evaluated. The serum HSP70 level in patients infected with HCV and normal individuals were detected by ELISA. The relationship between anti-HCV antibody and HSP70 was evaluated. Peripheral blood mononuclear cells (PBMCs) were activated by HSP70-HCV peptide complex and then 4 h 51Cr release assay were used to detect the killer activity of CTLs. Detection rates of HSP70 were 82.1% (22/28) and 18.8% (9/48) in patients with anti-HCV antibody and in normal individuals, resp. There was significant correlation between the detection rate of HSP70 and HCV infection ($\chi 2=28.77$, P<0.01). The level of serum HSP70 in patients infected with HCV was markedly more higher than that in normal individuals. CTLs from one patient induced by HSP70-HCV C region peptide (DLMGYIPAV) complex could lyse autologous B lymphoblastoid cell lines (BLcLs) with killer rate of 37.8%, whereas CTLs induced by peptide alone could not lyse autologous BLcLs cells. HCV infection can induce over expression of HSP70. HSP70 may have the action of enhancing presentation of HCV epitope peptide and promoting clearance cells infected with HCV.

IT 215295-45-7

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HSP70-HCV C region peptide complex cytotoxicity in patients with hepatitis C infection)

L2 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 13 Apr 2001

ACCESSION NUMBER: 2001:265271 CAPLUS

DOCUMENT NUMBER: 134:285564

TITLE: Pharmaceutical composition comprising an antigen

INVENTOR(S): Fleitmann, Julia-Kristina; Mattner, Frank;

Buschle, Michael; Melling, Jack

PATENT ASSIGNEE(S): Cistem Biotechnologies G.m.b.H., Austria

SOURCE: PCT Int. Appl., 20 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PA'	TENT	NO.			KIN	D	DATE			APP	LICAT	DATE				
		A2 200104 A3 200112				,	WO 2	2000-								
"0		AU,	BR,	CA,	CN,	CZ,		ID,	•		•	•	-	-	NZ	, PL,
	RW:	AT,		CH,											LU	, MC,
AT	9901				Α		2001	0715		AT :	1999-	1680				19991001
	4087															
EP	1218	031			A2		2002	0703		EP 2	2000-	9693	87			20001002
		AT,		CH,	DE,											, MC,
us	2003	•	•	,			2003	0529		us 2	2002-	1148	23			20020401
	2005										2005-					20050317
PRIORIT										AT :	1999-	1680			A	19991001
									(wo :	2000-	EP96	57	,	W .	20001002
										us 2	2002-	1148	23	,	A1	20020401

AB The inventions discloses a pharmaceutical composition comprising an antigen, an immunostimulating substance selected from neuroactive compds., hormones, compds. having a growth hormone activity, and mixts. thereof, and a polycationic polymer.

IT 215295-45-7

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (pharmaceutical composition comprising an antigen)

L2 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 03 Mar 2000

ACCESSION NUMBER: 2000:145039 CAPLUS

DOCUMENT NUMBER: 132:206926

TITLE: Modified HCV peptide vaccines

INVENTOR(S): Berzofsky, Jay A.; Sarobe, Pablo; Pendleton, C.

David; Feinstone, Stephen M.; Arichi, Tatsumi;

Major, Marian E.

PATENT ASSIGNEE(S): United States Dept. of Health and Human Services,

USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.					KIN	D	DATE		i	APPL:	DATE					
200001110					A1 20000302 C2 20020822				1	WO 1	19990817					
WO		AE,	AL,	AM,	AT,	AU,		BA,	•	•	-	-	-			-
		IL,	IN,	IS,	JP,	KE,	KG, MW,	KP,	KR,	KZ,	LC,	LK,	LR,	LS,	LT,	LU,

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SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA,
             ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
             CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
    AU 9957767
                                20000314
                                           AU 1999-57767
                                                                    19990817
                          A1
                          Α1
                                20010613
                                           EP 1999-945074
                                                                    19990817
    EP 1105496
            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
             PT, IE, SI, LT, LV, FI, RO
                                20040203
                                            US 2001-763260
                                                                    20011019
                          B1
                                            US 2004-770117
                                                                    20040202
                                20050616
    US 2005129705
                          A1
                                            US 1998-97446P
                                                                   19980821
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PRIORITY APPLN. INFO .:
                                            WO 1999-US18674
                                                                   19990817
                                            US 2001-763260
                                                                A3 20011019
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The present invention provides (1) an isolated peptide having the AΒ amino acid sequence DLMGYIPAV, (SEQ ID NO: 1); (2) an isolated HCV core polypeptide comprising an $L \rightarrow A$ substitution at amino acid position 139; (3) an isolated HCV core polypeptide having the amino acid sequence of SEQ ID NO: 2; and (4) a fragment of an HCV core polypeptide having fewer amino acids than the entire HCV core polypeptide and comprising the amino acid sequence SEQ ID NO: 1. provided are nucleic acids which encode the peptides and polypeptides of this invention, vectors comprising the nucleic acids of this invention and cells comprising the vectors and nucleic acids of this invention. The present invention further provides methods of producing an immune response in a subject and/or treating or preventing HCV infection in a subject, comprising administering to the subject, or to a cell of the subject, any of the compns. of this invention. The present invention also provides methods for determining a viral load and prognosis of a subject diagnosed with hepatitis C virus infection.

IT 260232-79-9

RL: PRP (Properties)

(amino acid sequence; modified HCV peptides as vaccines and for determination of virus load or prognosis of HCV infection)

IT 215295-45-7

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(modified HCV peptides as vaccines and for determination of virus load or prognosis of HCV infection)

REFERENCE COUNT:

THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

6

ED Entered STN: 30 Sep 1998

ACCESSION NUMBER: 1998:618237 CAPLUS

DOCUMENT NUMBER: 129:329617

TITLE: Enhanced in vitro potency and in vivo

immunogenicity of a CTL epitope from hepatitis C

virus core protein following amino acid replacement at secondary HLA-A2.1 binding

positions

AUTHOR(S): Sarobe, Pablo; Pendleton, C. David; Akatsuka,

Toshitaka; Lau, Daryl; Engelhard, Victor H.;

Feinstone, Stephen M.; Berzofsky, Jay A.

CORPORATE SOURCE: Molecular Immunogenetics and Vaccine Research

Section, Metabolism Branch, National Cancer Institute, National Institutes of Health,

Bethesda, MD, 20892, USA

SOURCE: Journal of Clinical Investigation (1998), 102(6),

1239-1248

CODEN: JCINAO; ISSN: 0021-9738 Rockefeller University Press

PUBLISHER: Rockefel
DOCUMENT TYPE: Journal
LANGUAGE: English

Since the natural immune response to hepatitis C virus (HCV) is often unable to clear the infection, to enhance immunogenicity we studied substituted peptides from an HCV cytotoxic T lymphocyte (CTL) epitope (C7A2) from a conserved region of the HCV core protein (DLMGYIPLV) recognized by CTL lines from HLA-A2.1+ HCV-infected patients and HLA-A2.1 transgenic mice. HLA-A2.1 binding, human and murine CTL recognition, and in vivo immunogenicity (using mice transgenic for human HLA-A2 in lieu of immunizing humans) were analyzed to define peptides with enhanced immunogenicity. Peptides substituted at position 1 showed enhanced HLA-A2 binding affinity, but paradoxically poorer immunogenicity. A peptide with Ala substituted at position 8 (8A) showed higher HLA-A2 binding affinity and CTL recognition and was a more potent in vivo immunogen in HLA-A2-transgenic mice, inducing higher CTL responses with higher avidity against native C7A2 than induced by C7A2 itself. These results suggest that peptide 8A is a more potent in vitro antigen and in vivo immunogen than C7A2 and may be useful as a vaccine component. They provide proof of principle that the strategy of epitope enhancement can enhance immunogenicity of a CTL epitope recognized by human CTL.

IT 215295-45-7P

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)

(enhanced potency and immunogenicity of CTL epitope from hepatitis C virus core protein following amino acid replacement at secondary HLA-A2.1 binding positions)

REFERENCE COUNT:

THERE ARE 69 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

69

ED Entered STN: 17 Nov 1997

ACCESSION NUMBER: 1997:725337 CAPLUS

DOCUMENT NUMBER: 128:33617

TITLE: Immunological significance of cytotoxic T

lymphocyte epitope variants in patients

chronically infected by the hepatitis C virus

AUTHOR(S): Chang, Kyong-Mi; Rehermann, Barbara; Mchutchison,

John G.; Pasquinelli, Claudio; Southwood, Scott;

Sette, Alessandro; Chisari, Francis V.

CORPORATE SOURCE: Department of Molecular & Experimental Medicine,

The Scripps Research Institute, La Jolla, CA, CA

92037, USA

SOURCE: Journal of Clinical Investigation (1997), 100(9),

2376-2385

CODEN: JCINAO; ISSN: 0021-9738

PUBLISHER: Rockefeller University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

This study was performed to test the hypothesis that cytotoxic T lymphocyte (CTL) selection of hepatitis C virus (HCV) escape variants plays a role in HCV persistence. The peripheral blood CTL responsiveness of patients with well-established chronic hepatitis C to a panel of 10 prototype HCV peptides (genotype 1a) was compared with the corresponding sequences encoded by the infecting viruses in each patient. Variant viral peptide sequences were threefold more frequent in the presence of a CTL response than in its absence, and CTL responses were detected nearly twice as often in association with variant rather than with prototype viral peptide sequences. Furthermore, over half of the patients were infected with potential CTL escape variants that contained nonimmunogenic and noncross-reactive variant peptides many of which displayed reduced HLA-binding affinity. Surprisingly, follow up anal. over a period of up to 46 mo revealed that, in contrast to the relatively high frequency of escape variants initially observed, the subsequent emergence rate of CTL escape variants was very low. Interestingly, the one escape variant that was detected proved to be a CTL antagonist. Collectively, these observations suggest that CTL selection of epitope variants may have occurred in these patients before their entrance into the study and that it may have played a role in HCV persistence. The low apparent rate of ongoing CTL selection in chronically infected patients, however, suggests that if CTL escape occurs during HCV infection it is probably an early event.

IT 199533-14-7P

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)

(cytotoxic T lymphocytes of humans with chronic hepatitis C virus infection reactivity with viral variant epitope)

REFERENCE COUNT:

THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'MEDLINE' ENTERED AT 16:49:08 ON 24 JAN 2006

40

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FILE 'REGISTRY' ENTERED AT 16:48:20 ON 24 JAN 2006 L1 4 SEA ABB=ON PLU=ON DLMGYIPAV/SQSP

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FILE 'CAPLUS' ENTERED AT 16:48:58 ON 24 JAN 2006
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FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:49:08 ON 24 JAN 2006 L3 0 SEA ABB=ON PLU=ON L1

FILE 'HOME' ENTERED AT 16:49:15 ON 24 JAN 2006

FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 23 JAN 2006 HIGHEST RN 872490-64-7 DICTIONARY FILE UPDATES: 23 JAN 2006 HIGHEST RN 872490-64-7

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TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

* The CA roles and document type information have been removed from * the IDE default display format and the ED field has been added, * effective March 20, 2005. A new display format, IDERL, is now * available and contains the CA role and document type information. * *

Structure search iteration limits have been increased. See HELP SLIMI for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

FILE CAPLUS

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FILE COVERS 1907 - 24 Jan 2006 VOL 144 ISS 5 FILE LAST UPDATED: 23 Jan 2006 (20060123/ED)

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FILE MEDLINE

FILE LAST UPDATED: 21 JAN 2006 (20060121/UP). FILE COVERS 1950 TO DA

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details on the 2005 reload, enter HELP RLOAD at an arrow promt (=>). See also:

http://www.nlm.nih.gov/mesh/

http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05 med data changes.ht

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05 2006 MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate

FILE BIOSIS

FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 19 January 2006 (20060119/ED)

FILE EMBASE

FILE COVERS 1974 TO 19 Jan 2006 (20060119/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE HOME

Score

Result

Hepatitis HCV-1 der Human HCV

Peptide f T cell ep HLA Class Hepatitis

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HCV type Hepatitis Hepatitis Hepatitis
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Post-processing:

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Title: Perfect score:

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Scoring table:

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response fragments of the Hepatitis C virus (HCV) core polypeptide can be used to elicit an immune response. A cytotoxic T-lymphocyte (CTL) cesponse is present in patients acutely and chronically infected by HCV.

CTL's recognise viral antigens as peptides presented by Class I molecules of the major histocompatability complex (MHC). These peptide antigens are cypically and acids long. These peptide antigens rypically have a sequence pattern or motif depending upon which particular MHC antigen they are bound and presented by. The motifs are based on the presence in they are bound and presented by. The motifs are based on the presence in they are bound and machor residues, responsible for interactions care poptide and mHC molecule, as well as other secondary position between peptide and MHC molecule, as well as other secondary position charges within the peptide sequence can enhance the immune response. Peptides derived from the HCV core polypeptide having substituted amino acid suthin their sequence can enhance the immune response against HCV. They can therefore be used as a vaccine or for treating HCV infection. This peptide is a fragment of the substituted HCV core polypeptide and comprises the region of amino acids within that polypeptide from position 132 to position 140 which contains the amino acid substitution
Aaj03787 Hepatitis
Aaj04086 Hepatitis
Abg79901 MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus polypeptides is useful as a vaccine for treating
Hepatitis C virus infection and for activating cytotoxic T lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agretope; anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC; Major histocompatibility complex; vaccine; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substituted hepatitis C virus core polypeptide antigenic fragment.
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                                                                                                                                                                                                                                                                                                                             AAY82996 standard; peptide; 9 AA
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Hepatitis C virus; (HCV).
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                                                                                                                                                                                                                                                                                      Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Score 47; DB 3; Length 9;
Pred. No. 2e+06;
0; Mismatches 0; Indels
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                                                                                                                                                           AAB82052 standard, peptide, 9 AA.
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                                                                                                                                                                                                                                                             HCV antigen, core 132-140.
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22-JUN-2001
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Zettlmeissl G;

Zauner W,

Lingnau K,

Klade C,

Buschle M, Frisch J, (INTE-) INTERCELL AG

WPI; 2005-101792/11.

11-JUL-2003; 2003EP-00450171. 09-JUL-2004; 2004WO-EP007540

Hepatitis C virus HCV vaccine useful for preparation of medicament for prevention and treatment of infection with HCV, comprises two epitopes from different hotspot epitope containing specific peptide.

Example 4; Page 33; 59pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a vaccine (V1) for preventing viral infections comprises an antigen, a peptide comprising a sequence R1-XZXZXXZX-R2, where N is 3-7 (preferably 5); X is positively charged natural and/or non natural amino acid residue; Z is amino acid residue chosen from Leu, Val, Ile, Phe and/or Trp; R1 and R2 is chosen from H. -NR2, -COCH3, COCH3, a peptide with up to 20 amino acid residues or peptide reactive group or peptide linker with or without peptide, and X-R2 may be an amide, ester or thioester of the C-rerminal amino acid residue of the peptide (Peptide A); and an immunostimulatory oligodeoxymucleic acid molecule (DND), (V1) is useful for preventing viral infections cost by influenza virus, HBV, HCV, HPV or JBV. A mixture of Peptide A and a I-/U-ODN (PI) is useful for improving the protective efficacy of (V1). This sequence corresponds to peptide p87 derived from hepatitis C virus protein and used in the vaccine of the invention to generate HCV-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
   virucide; anti-HIV; hepatotropic; antiinflammatory; vaccine;
viral infection; antigen; immunostimulatory oligodeoxynucleic acid;
influenza virus; HBV; HIV; HCV; HPV; JBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine useful for preventing viral infections, comprises anti
peptide and immunostimulatory oligodeoxynucleic acid molecule.
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                                                                                                                                                                                                                                                                                                                                      Buschle M, Habel A, Fritz J, Prinz K, Lingnau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV-derived vaccine peptide p87 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 27; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type 1 cellular response in mice
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                                                                                                                                                                                                                           24-MAR-2003; 2003EP-00450072.
11-APR-2003; 2003EP-00450084.
11-JUL-2003; 2003EP-00450171.
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Matches 9; Conserv
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Sequence 9 AA;

The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. As included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing the epitopes by an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.

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Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection; gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zettlmeissl G;
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                                           100.0%; Score 47; DB 9; Length 9; larity 100.0%; Pred. No. 2e+06; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lingnau K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADV96796 standard; peptide; 9 AA.
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12-MAR-2004; 2004EP-00450062.
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Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection; gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.

Hepatitis C virus

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WO2005004910-A2

20-JAN-2005

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optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The presents equence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus HCV vaccine useful for preparation of medicament prevention and treatment of infection with HCV, comprises two epito from different hotspot epitope containing specific peptide.
                                                                                                       100.0%; Score 47; DB 9; Length 9;
100.0%; Pred. No. 2e+06;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                     HCV-derived vaccine peptide p87 #2.
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                                                                                                                                                                                                                                                                             ADV96886 standard; peptide; 9 AA.
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12-MAR-2004; 2004EP-00450062.
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                                                                                                                     Similarity 100.
9; Conservative
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les 9; Conserv
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                                                                                                                                                                    1 DLMGYIPAV
                                                                                                                                                                                                 DLMGYIPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus
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                                                                             Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                           ADV96886;
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Best Local
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Matches
                                                                                                                                       Matches
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ID ADV9
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                                                                      The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing the epitopes by an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.
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gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
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    two epitopes
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 treatment of infection with HCV, comprises thotspot epitope containing specific peptide.
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                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV96890 standard; peptide; 9 AA.
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                                              Claim 5; Page 52; 59pp; English
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12-MAR-2004; 2004EP-00450062.
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Best Local Similarity 100.0.
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    prevention and from different
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The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing the epitopes by an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and itse halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicaement for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.
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ilarity 100.0%; Pred. No. 2e+06;
Conservative 0; Mismatches 0
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two epitopes

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Zettlmeissl

Zauner W,

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Buschle M, Frisch J,
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Best Local Similarity
                                   Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing from formic acid, an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.
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                                                                                                                                  Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection; gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
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                                                                                                                                                                                                                                                                                                          Lingnau K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                               ADV96961 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                          Klade C,
                                                                                                              HCV-derived vaccine peptide 87.
                                                                                                                                                                                                                               09-JUL-2004; 2004WO-EP007540.
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                                                                                         (first entry)
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                                                                                                                                                                  Hepatitis C virus.
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Matches
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The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing the epitopes by an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide
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Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection; gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
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12-MAR-2004; 2004EP-00450062.
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12-MAR-2004; 2004EP-00450062.
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Hepatitis C virus polypeptides is useful as a vaccine for treating
Hepatitis C virus infection and for activating cytotoxic T lymphocytes.
                                              Claim 2, Page 71-72, 78pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ty-2 associated peptide H50.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 191 AA;
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                                                                                                                                                                                                    The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing from formic acid, acetic acid, propionic acid, butyric acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV epitope peptide derived from a hotspot epitope, used as a vaccine.
                                                                                                        Hepatitis C virus HCV vaccine useful for preparation of medicament for prevention and treatment of infection with HCV, comprises two epitopes from different hotspot epitope containing specific peptide.
                                              Zettlmeissl G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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anchor residue, cytotoxic T lymphocyte, CTL, immune response, MHC;
Major histocompatibility complex, vaccine, treatment.
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                                              Zauner W,
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                                              Lingnau K,
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                                                                                                                                                                         Example 5; Page 37; 59pp; English.
                                           Klade C,
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Best Local Similarity luv.
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                                             Buschle M, Frisch J,
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               (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DLMGYIPAV 9
                                                                           WPI; 2005-101792/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DLMGYIPAV
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200011186-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1998;
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Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be used to elicit an immune response. A cyctocxic T-lymphocyce (CTL) response is present in patients acutely and chronically infected by HCV.

CTL's recognise viral antigens as peptides presented by Class I molecules of the major histocompatability complex (MHC). These peptide antigens are cypically along and acids long. These peptide antigens typically have a sequence pattern or motif depending upon which particular MHC antigen they are bound and presented by. The motifs are based on the presence in they are bound and presented by. The motifs are based on the presence in they are bound and presented by. The motifs are based on the presence in they are postide and anchor residues, responsible for interactions between peptide and mHC molecule, as well as other secondary position to that may help to stabilise the interaction. Thus, single amino acid changes within the peptide sequence can enhance the immune response. Peptides derived from the HV core polypeptide having substituted amino acid acids within their sequence, specifically a a hepatitis C virus core polypeptide comprising an L to an A substitution at amino acid position 139 enhance the immune response against HVV. They can therefore be used as a vaccine or for treating HCV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 47; DB 3; Length 191; 100.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0, Indels
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Synthetic peptide A86 derived from a conserved region of HCV.

17-JUN-2004 (first entry)

ADL25899;

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ADL25899 standard; peptide; 15 AA.

HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

13-SEP-2002; 2002AT-00001376. 27-FEB-2003; 2003WO-EP002005. 11-JUL-2003; 2003EP-00450171.

(INTE-) INTERCELL AG

27-AUG-2003; 2003WO-EP009482.

WO2004024182-A2.

Synthetic

25-MAR-2004

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Epitope mapping; vaccine, T-cell; Hepatitis C virus infection; infection; gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a Hepatitis C virus (HCV) vaccine (VA) comprising at least two epitopes, each from a different hotspot epitope, where a hotspot epitope is defined as an epitope containing peptide having specific sequences. Also included is the preparation of VA, involving chemically synthesizing the two epitopes of VA, solubilizing the epitopes by an aqueous solution containing an organic acid chosen from formic acid, acetic acid, propionic acid, butyric acid and its halogenated or hydroxylated forms, mixing the solubilized epitopes and optionally lyophilizing the mixed epitopes. The vaccine is useful for the preparation of a medicament for the prevention and treatment of an infection with HCV. The present sequence is an HCV hotspot epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus HCV vaccine useful for preparation of medicament for prevention and treatment of infection with HCV, comprises two epitopes from different hotspot epitope containing specific peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zettlmeissl G;
                                                                                                 Gaps
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vaccine. This sequence represents a Ty-2 associated peptide.
                                                                                               1; Indels
                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zauner W,
                                                              Score 43; DB 8;
Pred. No. 2e+06;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lingnau K,
                                                                                                                                                                                                                                                                                                                                HCV T-cell epitope hotspot peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Misc-difference 8
                                                                                                                                                                                                                                    ADV96979 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 51; 59pp; English.
                                                           Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-2004; 2004WO-EP007540.
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12-MAR-2004; 2004EP-00450062
                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buschle M, Frisch J,
                                                                                                                          1 DLMGYIPAV 9
                                                                                                                                                      1 DLMGYIPVV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2005004910-A2.
                                 Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13 AA;
                                                                                                                                                                                                                                                                                                    07-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                           Isolating Hepatitis C Virus peptides (HPs) which have a binding capac: to a MRC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                             Mattner F, Otava O, Vytvytska O;
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Pred. No. 0.11;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 30; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                           Habel A, Klade C,
Zinke S, Kirlappos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL25904 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLMGYIPVV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLMGYIPAV 9
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-269899/25.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                          Zauner W,
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Matches
RESULT 15
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ID ADL2
XX
AC ADL2
XX
DT 17-C
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DB Synt
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Gaps

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1; Indels

Score 43; DB 9; Length 13; Pred. No. 0.093; 0; Mismatches 1; Indels

91.5%;

DLMGYIPAV S

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The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPS). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (HPS) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.
                                                                                                                                                      Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
                                                                                  Vytvytska 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic peptide A87 derived from a conserved region of HCV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.5%; Score 43; DB 8; Length 15; 88.9%; Pred. No. 0.11; ive 0; Mismatches 1; Indels
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                                                                                  otava O,
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H;
                                                                                 Mattner F,
                                                                                                                                                                                                                                   Example 1; Page 30; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL25900 standard; peptide; 15 AA.
                                                                                  Habel A, Klade C, M
Zinke S, Kirlappos H;
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27-FEB-2003; 2003WO-EP002005.
11-JUL-2003; 2003EP-00450171.
13-SEP-2002; 2002AT-00001376.
27-FEB-2003; 2003WO-EP002005.
11-JUL-2003; 2003EP-00450171.
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                                                       (INTE-) INTERCELL AG
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                                                                                                                              WPI; 2004-269899/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DLMGYIPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 8, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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                                                                                  Buschle M,
                                                                                                   Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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ADL25900
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                                                                                                                                                                                                                                                                                                                                     capacity
                                                                                                                                                                                                                                                                                                                                 Isolating Hepatitis C Virus peptides (HPs) which have a binding capac: to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                               Mattner F, Otava O, Vytvytska O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
             HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
major histocompatibility complex; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
major histocompatibility complex; human leukocyte antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptide A92 derived from a conserved region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 8, Pred. No. 0.11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 30; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL25905 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                            Zinke S, Kirlappos H;
                                                                                                                                                                                                                                                                Klade C,
                                                                                                                                                                       13-SEP-2002; 2002AT-00001376.
27-FEB-2003; 2003WO-EP002005.
11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003; 2003WO-EP009482
                                                                                                                                             27-AUG-2003; 2003WO-EP009482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DLMGYIPVV 10
                                                                                                                                                                                                                                                             Habel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLMGYIPAV 9
                                                                                                                                                                                                                                 (INTE-) INTERCELL AG
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                                                                                 WO2004024182-A2.
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                                                                                                                25-MAR-2004
                                                                                                                                                                                                                                                             Buschle M,
                                                       Synthetic
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The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPs). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for visolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the reells, a T cell clone or a T cell population or preparation. The T cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.
to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.
                                                                                                  Example 1; Page 30; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15
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Score 43; DB 8; Length 15; Pred. No. 0.11;
                                  1; Indels
                                 0; Mismatches
              91.5%;
88.9%;
Ouery Match
Best Local Similarity 86..
8, Conservative
                                                                        DLMGYIPVV 14
                                                    DLMGYIPAV 9
                                                    н
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ADL25901 standard; peptide; 15 AA.
RESULT 18
ADL25901
ID ADL25
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(first entry) 17-JUN-2004 ADL25901;

Synthetic peptide A88 derived from a conserved region of HCV.

HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

Synthetic

WO2004024182-A2

25-MAR-2004

27-AUG-2003; 2003WO-EP009482

13-SEP-2002; 2002AT-00001376. 27-FEB-2003; 2003WO-EP002005. 11-JUL-2003; 2003EP-00450171.

(INTE-) INTERCELL AG

Vytvytska Otava O, Mattner F, Kirlappos H; Klade C, Habel A, Zinke S, Buschle M, Zauner W,

WPI; 2004-269899/25.

Isolating Hepatitis C Virus peptides (HPB) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

Example 1; Page 30; 73pp; English.

The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPs). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T

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cells, a T cell clone or a T cell population or preparation is useful identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.
                                                                                                                              Gaps
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                                                                                                 Score 43; DB 8; Length 15; Pred. No. 0.11;
                                                                                                                              1; Indels
                                                                                                                            0; Mismatches
                                                                                              91.5%;
                                                                                                                            8; Conservative
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                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                DLMGYIPVV
                                                                                                                                                       1 DLMGYIPAV
                                                                      Sequence 15 AA;
 8888888
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RESULT 19

ADL25903 ID ADL2

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ADL25903 standard, peptide, 15 AA
                                        ADL25903;
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17-JUN-2004 (first entry)

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Gaps

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Synthetic peptide A90 derived from a conserved region of HCV.

HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

Synthetic.

WO2004024182-A2

25-MAR-2004.

27-AUG-2003; 2003WO-EP009482.

13-SEP-2002; 2002AT-00001376. 27-FEB-2003; 2003WO-EP002005. 11-JUL-2003; 2003EP-00450171.

(INTE-) INTERCELL AG

Vytvytska Otava O, Mattner F, Kirlappos H; Klade C, Habel A, Zinke S, Buschle M, Zauner W,

ö

WPI; 2004-269899/25

capacity Isolating Hepatitis C Virus peptides (HPs) which have a binding capacito a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

Example 1; Page 30; 73pp; English

The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPB). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (HPB) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T cells a T cell clone or a T cell population or preparing a useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic from a conserved region of HCV. derived peptide

Sequence 15 AA;

Gaps ö Length 15; Indels ; DB 8; 91.5%; Score 43; DB 8; 88.9%; Pred. No. 0.11; iive 0; Mismatches 8; Conservative Local Similarity Query Match Best Loca Matches

1 DLMGYIPAV 9

8

Vytvytska 0;

Otava O,

RESULT 20

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The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPB). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (HPB) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; antigen; diagnosis; reagent; agglutination.
Synthetic peptide 1649 derived from a conserved region of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.5%; Score 43; DB 8; Length 36; 88.9%; Pred. No. 0.29; ive 0; Mismatches 1; Indels
                                   HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide derived from a conserved region of HCV
                                                                                                                                                                                                                                                                                                                                                           Klade C, Mattner F,
Kirlappos H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR52735 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32; 73pp; English.
                                                                                                                                                                                                                                               13-SEP-2002; 2002AT-00001376.
27-FEB-2003; 2003WO-EP002005.
11-JUL-2003; 2003EP-00450171.
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                                                                                                                                                                                                           27-AUG-2003; 2003WO-EP009482.
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                                                                                                                                                                                                                                                                                                                                                               Buschle M, Habel A,
Zauner W, Zinke S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DLMGYIPAV 9
                                                                                                                                                                                                                                                                                                                           (INTE-) INTERCELL AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLMGYIPVV
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                                                                                                                                 WO2004024182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP06102273-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1995
                                                                                                                                                                       25-MAR-2004
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                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                   Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR52735;
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AAR52735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (HPB). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (HPB) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epicopes or for preparation is useful for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                 Synthetic peptide A89 derived from a conserved region of HCV.
                                                                                                                                                                                                                                                                       HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
major histocompatibility complex; human leukocyte antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 8; Length 15;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otava O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klade C, Mattner F,
Kirlappos H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 30; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL26466 standard; peptide; 36 AA.
                                                                                                                 ADL25902 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2002; 2002AT-00001376.
27-FEB-2003; 2003WO-EP002005.
11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-2003; 2003WO-EP009482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
 molecule by separatin
bind to the molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Habel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinke S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-269899/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLMGYIPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DLMGYIPUV
                                                                                                                                                                                                                                                                                                                                                                   WO2004024182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 AA;
                                                                                                                                                                                             17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buschle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zauner W,
                                                                                                                                                                                                                                                                                                                               Synthetic.
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RESULT 21
ADL26466
ID ADL26
XX
AC ADL26
XX
DT 17-JU

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Gape

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Gарв

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92JP-00250027.

18-SEP-1992;

(TOKU) TOKUYAMA SODA KK

WPI; 1994-161280/20. N-PSDB; AAQ62688.

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Protein contg. non-A non-B hepatitis antigen fragment - prepd. by culturing transformants transformed by vector contg. base sequence coding specified aminoacid sequences, used for detecting hepatitis.
                                                                                                                                                                                                                                                                                                       non-A non-B hepatitis virus, NANBH; hepatitis C virus; HCV; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a non-A non-B hepatitis virus (NANBH) or hepatitis C virus (HCV) antigen, useful for diagnosis or detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capsid protein, attenuated vaccine, virucide, antinflammatory, hepatotropic, yellow fever, Japanese encephalitis, dengue, classical swine fever; bovine viral diarrhoea; hepatitis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 188;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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     Pred. No. 1.6;
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Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                   AAW41753 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV type 2 capsid protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB71257 standard; protein; 190 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          91JP-00354708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90JP-00412020
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
                                                                                                                                                                                                                                    22-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                    Hepatitis C virus antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIM/) SHIMOTONO K. (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                132 DLMGYIPVV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 DLMGYIPVV 148
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                                                  1 DLMGYIPAV 9
                                                                                                                                                                                                                                                                                                                          diagnosis; detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-260858/33.
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                                                                                                                                                                                                                                                                                                                                                      Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1991;
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18-NOV-2002
                                                                                                                                                                                                    AAW41753;
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                                                                                                                                                                                               An new immunological agglutination reaction reagent for the diagnosis of hepatitis C uses a HCV antigen polypeptide subjected to heat-treatment. The HCV antigen active polypeptide contains one of the polypeptides given in AAR52735-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The polypeptide provokes an antibody response to hepatitis C virus (HCV). It can be produced in large quantities by fusing this coding sequence to the beta-galactoopidase gene and then transforming B. coll with the resulting construct. The E. coli can then be cultured and the fusion protein expressed and recovered from the supernatant. The polypeptide reacts specifically with anti-HCV antibodies and can be used for the identification of such. It can therefore be used to identify individuals infected with HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; detection; infection; fusion protein; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \ensuremath{\mathsf{HCV}} antigen active fusion polypeptide - for the detection of anti-HCV antibodies.
                                                                                                           Immunological agglutination reagent for the diagnosis of hepatitis C comprising hepatitis C virus antigen polypeptide.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; Length 168;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 168;
                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Antigenic fragment of hepatitis C virus.

fermentation; antigen.

Hepatitis C virus,

JP06046872-A.

22-FEB-1994.

(first entry)

17-OCT-1994

AAR49831;

92JP-00198806 92JP-00198806

24-JUL-1992; 24-JUL-1992; (TOKU) TOKUYAMA SODA KK

1994-097028/12.

N-PSDB; AAR4983

Claim 1; Page 9; 15pp; Japanese.

Sequence 168 AA;

Query Match

AAR49831 standard; protein; 168 AA.

RESULT 23 AAR4983.

0; Mismatches

8; Conservative

132 DLMGYIPVV 140

1 DLMGYIPAV 9

ò g G

91.5%;

Query Match Best Local Similarity

Sequence 168 AA;

Claim 2-3; Page 15-16; 18pp; Japanese.

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Gaрв

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94US-00290665
                     (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US SEC DEPT HEALTH
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                  132 DĽMGYÍPVV 140
                                                                                                                                                                                                                                                                                                                                           1 DLMGYIPAV 9
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                                            Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-139709/14.
                                                                  WPI; 1996-139709/14
                                                                                                                                                                                                                                                                                                       Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                               N-PSDB; AAT16634.
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                                                                                                                                                                                                                                                                      Sequence 191 AA;
                                                                                                                                                                                                                                                 HCV infection
15-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatitis.
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                                            Bukh J,
                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                           This invention describes a novel attenuated flavivirus live vaccine comprising a flavivirus mutant that has a deletion of at least 4 consecutive amino acids from the capaid protein, provided that the C. terminal hydrophobic region is not affected by the deletion. The vaccine of the invention has virucide, antinflammatory and hepatotropic activity. The attenuated vaccine, and similar nucleic acid vaccines that encode the mutated capaid protein, are useful for protection against a wide range of flavivirus diseases, e.g. yellow fever, Japanese encephalitis, dengue, classical swine fever, bovine viral diarrhoea and hepatitis C. The specified deletion: (i) produces a reliably attenuated virus that does not revert to virulence; (ii) is exactly defined and does not effect immune responses to important proteins; and (iii) can not generate a nontarus virus by recombination. The mutant viruses aliminate the need to produce large amounts of infectious virulent viruses, and can be produced with less expense. The protective response to flavivirus lasts asymificantly longer than that to killed vaccines. This sequence represents a fragment of the capsid protein from Hepatitis c virus (HCV) type 1 described in the disclosure of the invention. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                         Attenuated flavivirus live vaccine, useful for protection against e.g. yellow fever, comprises virus with attenuating deletion of amino acids from the capsid protein.
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Pred. No. 1.8;
0; Mismatches
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                                                                                                                                                                                                                         Disclosure, Fig 2; 30pp; German.
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                                            11-FEB-2002; 2002WO-AT000046.
                                                                  21-FEB-2001; 2001AT-00000272
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                                                                                                                                                   WPI; 2002-667064/71
                                                                                                                             Mandl C;
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Best Local Similarity
Matches 8; Conserv
                                                                                         (HEIN/) HEINZ F X. (MAND/) MANDL C.
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WO200266621-A1
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                     29-AUG-2002
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                                                                                                                             Heinz FX,
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                                                                                                                                                                                                DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                 AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated CDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used cto detect antibodies against HCV in serum, saliva, lymphocytes or other monounclear cells. The antibodies may be used in the prevention of
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                        Claim 4; Page 200-201; 340pp; English.
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Purcell RH;
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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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                                                                                                                               envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 1.8;
); Mismatches
                                                                                                Hepatitis C virus isolate DK8 core protein.
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        AAR92966 standard; protein; 191 AA.
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Best Local Similarity 88.9*,
8; Conservative
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                                                                                                                                              hepatitis.
                                       AAR92966;
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vaccines for immunising against HCV infection. The proteins may also used to detect antibodies against HCV in serum, saliva, lymphocytes or per mononuclear cells. The antibodies may be used in the prevention of
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Pred. No. 1.8;
0; Mismatches
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88.9%;
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N-PSDB; AAT16652.
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Best Local Similarity
Matches 8; Consery
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Best Local Similarity
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                                                                            Sequence 191 AA;
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15-AUG-1995;

RESULT 29 AAR92966

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22-FEB-1996

Length 191; Indels ö

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also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monounclear cells. The antibodies may be used in the prevention of HCV infection
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Pred. No. 1.8;
0; Mismatches
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Pred. No. 1.8;
0; Mismatches
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                                                                                                  Query Match
Best Local Similarity 85.,
8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukh J,
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                                                                                                                                                                                                                                     RESULT 32
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                                                                                                                                         DNA and amino acid sequence of HCV envelope 1 and core proteins determine HCV genotype and as vaccines against HCV infection.
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                                                                                                                                                                                                                                                                                                                                                           2; Length 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus isolate US10 core protein.
                                                                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No. 1
0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 199-200; 340pp; English.
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                                                                                                                                                                                 Claim 4; Page 223; 340pp; English
                                                                         Purcell RH;
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                                              (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     132 DLMGYIPVV 140
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                                                                       Miller RH,
                                                                                                  WPI; 1996-139709/14
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                                                                                                                N-PSDB; AAT16661.
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                                                                                                                                                                                                                                                                                                                                Sequence 191 AA
                                                                                                                                                                                                                                                                                                        HCV infection
                      15-AUG-1994;
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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 1.8;
); Mismatches
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                                                                                                                                                                                                                        Claim 4; Page 204-205; 340pp; English.
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                              94US-00290665
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                                                                                         Miller RH,
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N-PSDB; AAT16641.
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Best Local Similarity
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                                                                                                                                          N-PSDB; AAT16639
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                     HCV infection
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                            15-AUG-1994;
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Matches
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                                                                                                                                   envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 1.8;
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                                                                                                   Hepatitis C virus isolate DK11 core protein.
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        standard; protein; 191
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Query Match

Best Loc Matches

AAR92965

RESULT 34 AAR92965

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HCV; El;

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(INNO-) INNOGENETICS NV
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   RESULT 37
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useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunishing against HCV infection. The proteins may also be used to detect amulbodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                   El; envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 1.8;
0; Mismatches 1; Indels
                                                                                       Length 191;
                                                                                                            1; Indels
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Pred. No. 1.8;
0; Mismatches
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                           8; Conservative
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| 132 DLMGYIPVV 140
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Matches 8; Conserv
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                                                                     Sequence 191 AA;
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                                                  HCV infection
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                                                                                                                                                                             non-A non-B hepatitis virus; NANBH; hepatitis C virus; HCV; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a non-A non-B hepatitis virus (NANBH) or hepatitis C virus (HCV) antigen, useful for diagnosis or detection
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Pred. No. 1.8;
0; Mismatches
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AAW41755 standard, protein, 193 AA
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17-JUL-2001; 2001US-0305604P.
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88.9%;
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                                                                                                                                 Hepatitis C virus antigen.
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Best Local Similarity
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                                                                                                                                                                                                                                                   Hepatitis virus.
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The present invention describes a recombinant nucleic acid (I) comprising a nucleotide sequence encoding a protein having an avian lysozyme leader peptide, or its functional equivalent, joined to a Hepatitis C virus (HCV) envelope protein or its part. And odescribed: (I) a vector comprising the recombinant nucleic acid; (2) a host cell comprising the recombinant nucleic acid; (2) a host cell comprising the HCV envelope protein or its part in a host cell, comprising transforming the host cell with the recombinant nucleic acid or with the vector, where the host cell is capable of expressing the protein cited above. (I) has hepatotropic, virucide and antiinflammatory activities, and can be used
                                                                                                                                                                                                                                                                                                                                                                                 in gene therapy and vaccines. The recombinant nucleic acid is useful for efficient expression of Hepatitis C virus envelope proteins in eukaryotic cells, such as yeast cells. The HCV envelope proteins may be used as a vaccine, or for incorporation into an immunoassay for the detection of anti-HCV antibodies, and/or genotyping of HCV, for prognosing or monitoring of HCV disease, or as a therapeutic agent. The method is used for producing HCV envelope protein or its part in a host cell. AB084197 to AB084253 and ABP55528 to ABP55568 represent sequences used in the
                                                                            New recombinant nucleic acids for expressing Hepatitis C virus (HCV) envelope proteins in eukaryotic cells, comprising a sequence encoding protein having an avian lysozyme leader peptide joined to the HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide; antiinflammatory; gene therapy; vaccine.
                    Deschamps G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 6; Length 209;
Pred. No. 2;
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                  Depla E,
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                Bosman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention
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                                                                                                                                                                  Claim 5; Page 309-310; 319pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus protein SEQ ID NO:89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP55559 standard; protein; 209 AA.
              Van Broekhoven A,
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17-JUL-2001; 2001US-0305604P.
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                                             WPI; 2003-093095/08
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Best Local Similarity
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                                                                                                                                     envelope proteín.
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            Sablon E,
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WPI; 2003-093095/08.

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a nucleotide sequence encoding a protein having an avian lyaczyme leader peptide, or its functional equivalent, joined to a Hepatitis C virus (HCV) envelope protein or its part. Also described: (1) a vector comprising the recombinant nucleic acid; (2) a host cell comprising the recombinant nucleic acid; (3) a method for producing HCV envelope protein or its part in a host cell, comprising transforming the host cell with the recombinant nucleic acid or with the vector, where the host cell with the recombinant nucleic acid or with the vector, where the host cell with the recombinant nucleic acid or with the vector, where the host cell is capable of expressing the protein cited above. (1) has consider the host cell is capable of expressing the protein cited above. (1) has consider the host cell is capable of expressing the protein sin ensed is useful for efficient expression of Hepatitis C virus envelope proteins in enkaryotic cells, such as yeast cells. The HCV envelope proteins may be used as a vaccine, or for incorporation into an immunoassay for the detection of anti-HCV antibodies, and/or genotyping of HCV, for prognosing or anti-HCV antibodies, and/or genotyping of HCV, for prognosing or cells, monitoring of HCV disease, or as a therapeutic agent. The method is used for producing HCV envelope protein or its part in a host cell. ABQ84157 co ABQ84253 and ABB5528 to ABB5528 represent sequences used in the exemplification of the present invention
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                                                                                                                                      The present invention describes a recombinant nucleic acid (I) comprising
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New recombinant nucleic acids for expressing Hepatitis C virus (HCV) envelope proteins in eukaryotic cells, comprising a sequence encoding protein having an avian lysozyme leader peptide joined to the HCV.
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Pred. No. 2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus protein SEQ ID NO:94.
                                                                                            Claim 5; Page 308-309; 319pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP55564 standard; protein; 209 AA
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17-JUL-2001; 2001US-0305604P.
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-hes 8; Conservative
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                                                           envelope protein.
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The present invention describes a recombinant nucleic acid (I) comprising a nucleotide sequence encoding a protein having an avian lysozyme leader peptide, or its functional equivalent, joined to a Hepatitis C virus (HCV) envelope protein or its part. Also described: (I) a vector ecombinant nucleic acid; (2) a host cell comprising the recombinant nucleic acid; (2) a host cell comprising the creombinant nucleic acid or the vector; and (3) a method for producing HCV envelope protein or its part in a host cell; comprising transforming the host cell with the recombinant nucleic acid or with the vector; where the host cell is capable of expressing the protein cited above. (I) has hepatotropic, virucide and antiinflammatory activities, and can be used in gene therapy and vaccines. The HCV envelope proteins in eukaryotic efficient expression of Hepatitis C virus envelope proteins in eukaryotic cells, anch as yeast cells. The HCV envelope proteins may be used as a vaccine, or for incorporation into an immunoassay for the detection of anti-HCV antibodies, and/or genotyping of HCV, for prognosing or cells, and ABDSSSSS and ABDSSSSS Proteins in a host cell. ABQ84197 cto ABQ841231 and ABDSSSSS Proteins expresent invention
Claim 5; Page 313-314; 319pp; English.
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91.5%; Score 43; DB 6; Length 209;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels

15 DLMGYIPVV 23 1 DLMGYIPAV 9 ò 셤 completed: January 20, 2006, 22:40:13

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US-08-978-281A-42
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US-09-929-955-2
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Result No.

Post-processing:

Database

Total number of

Searched:

Title: Perfect score:

Sequence:

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protein

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Run on:

Scoring table:

Appi Appi Appi Appi Appi Appi

APP APP APP1 APP1 APP1

; OTHER INFORMATION: SYNTHETIC CONSTRUCT US-09-763-260-2 à 셤 ଚ 셤 ö OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e = OTHER INFORMATION: synthetic construct US-09-763-260-1 APPLICANT: The Government of the United States, as represented by the APPLICANT: Secretary, Dept. of APPLICANT: Bealth and Human Services APPLICANT: Beazofsky, Jay A. APPLICANT: Barzofsky, Jay A. APPLICANT: Barzofsky, Jay A. APPLICANT: Pendleton, C. David APPLICANT: Pendleton, C. David APPLICANT: Arichi, Tatsumi APPLICANT: Arichi, Tatsumi APPLICANT: Arichi, Tatsumi E. TITLE OF INVENTION: ModiFIED HCV PEPTIDE VACCINES FILE REFERENCE: 14014-0347/P CURRENT APPLICATION NUMBER: US/09/763,260 CURRENT APPLICATION NUMBER: US/09-119-119 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e = ö Query Match 100.0%; Score 47; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels ALIGNMENTS NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 PRIOR APPLICATION NUMBER: 60/097,446 PRIOR FILING DATE: 1998-08-21 Sequence 1, Application US/09763260 Patent No. 6685944 GENERAL INFORMATION: TYPE: PRT ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence 1 DLMGYIPAV 9 JS-09-763-260-1 -09-763-260-2 SEQ ID NO 1 LENGTH: 9

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                                                                                                                                                                                                                                                                    US-08-290-665A-178

Sequence 178, Application US/08290665A

Sequence 178, Application US/08290665A

GENERAL INFORMATION:

APPLICANT: BUTCH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: CORE GENES OF REAGENTS DERIVED FROM THESE

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF INVENTION: SEQUENCES 263

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                       100.0%; Score 47; DB 2; Length 191; 100.0%; Pred. No. 0.068;
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                                                                          0; Indels
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 10154

COMPUTER: READMALE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATIONG SYSTEM: PC-DGS/MS-DGS
SOFTWARE: WORDERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION MURBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY, AGRAY THORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-290-665A-179
; Sequence 179, Application US/08290665A
; Patent No. 5882852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 421792
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         individual isolate: US10
US-08-290-665A-178
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CITY: NEW YORK
STATE: NEW YORK
Query Match
Best Local Similarity 100.
                                                                                                                                                                       132 DLMGYIPAV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino a
STRANDEDNESS:
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ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE DOCKET NUMBER: 207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.5
Then 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homosapiens INDIVIDUAL ISOLATE: T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 DLMGYIPVV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unkno
TOPOLOGY: unknown
ORIGINAL SOURCE:
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US-08-290-665A-180

i Sequence 180, Application US/08290665A

patent No. 5882852

GENERAL INFORMATION:

APPLICANT: BURH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

ITILE OF INVENTION: NUCLEOTIDE AND DEDUCED

ITILE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

ITILE OF INVENTION: AND THE USE OF INEPATITIS C VIRUS

ITILE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 263

NUMBER OF SEQUENCES: 263

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154
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                                     NUCLEOTIDE AND DEDUCED
NUCLEOTIDE AND DEDUCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
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88.9%; Pred. No. 0.45;
tive 0; Mismatches 1; Indels
       GENERAL INCOMENT: BURGE, N. H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCES
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCES
TITLE OF INVENTION: AND THE USE OF REAGEN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 36,459
FILING DATE: 15-AUG-1994
CLASSIFICATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
TELEFAX: 421792
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: AND FORMATION
TOWNEY: CONTROLL
TOWNEY: CONTROLL
TYPE: AMINOWIN
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Best Local Similarity 88.9
Matches 8, Conservative
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INDIVIDUAL ISOLATE: T9
GENERAL INFORMATION:
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Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUTGH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLECTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORR GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 0.45;
0; Mismatches 1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
CONFUTER: IBM PC CONFATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 antino acids
TURENTHE OFFICE CHARACTERISTICS:
LENGTH: 191 antino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
COMPUTER: 10154
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IB PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NATA:
RPLING DATE: 15-AUG-1994
CLASSIFICATION: 435
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Gaps
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Sequence 184, Application US/08290665A

Sequence 184, Application US/08290665A

Patent No. 5882822

GENERAL INFORMATION:

APPLICANT: BUKH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS

TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE

TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1994
CLASSIFICATION 1435
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 758-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 191 amino acids TYPE: amino acid STRANBEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homosapiens
INDIVIDUAL ISOLATE: DK11
                                  132 DLMGYIPVV 140
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                                                                                                                       US-08-290-665A-183
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AND ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
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Pred. No. 0.45;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-290-665A-182

Sequence 182, Application US/08290665A

Sequence 182, Application US/08290665A

Sequence 182, Application US/08290665A

SERREAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLECTIDE AND DEDUCT
TITLE OF INVENTION: AMINO ACID SEQUENCES;
TITLE OF INVENTION: AMINO ACID SEQUENCES;
TITLE OF INVENTION: SEQUENCES IN DIAGNOS;
TITLE OF INVENTION: SEQUENCES IN DIAGNOS;
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECHONE: (212) 758-4800
TELECHONE: (212) 758-4800
TELEX: 421792
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T8
US-08-290-665A-181
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INFORMATION FOR SEQ ID NO: 182: SEQUENCE CHARACTERISTICS: LENGTH: 191 amino acids TYPE: amino acid STRANDEDNESS: unknown TOPOLOGY: unknown ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: US1
US-08-290-665A-182
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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FILING DATE: 15-AUG-1994
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US-08-290-665A-185
; Sequence 185, Application US/08290665A
; Patent No. 5802852
; GENERAL INFORMATION:
APPLICANT: BURH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPENDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
STREET: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPEY DISK
COMPUTER: ENORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFREECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATICON INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
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APPLICATION NUMBER: US/08/290,665A
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STREET: 345 PARK AVENUE
STAET: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 12-1
TELEX: 421792
INPORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
"nooloGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SW3
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CLASSIVATION NUMBER: 2226-4116

MARE: RICHARD W. BORNA

REPERENCY/COCKT NUMBER: 2226-4116

TELEPOWNINGCATION INFORMATION:
TOTAL INFORMATION INFORMATION:
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Sequence 206, Application US/08290665A
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Sequence 197, Application US/08290665A

Sequence 197, Application US/08290665A

Patent No. 5802825

Patent No. 5802825

Patent No. 5802825

TERE OF INVENTION: MULLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS

TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 263

CORRESPONDENCE ADDRESS:
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91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                             Score 43; DB 1; Length 191;
Pred. No. 0.45;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTONNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 32026-4116
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTRRISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                             Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homosapiens
INDIVIDUAL ISOLATE: DK13
                            ORGANISM: homosapiens
INDIVIDUAL ISOLATE: $83
US-08-290-665A-186
                                                                                                                                                                                                                                                                                                                                                                  132 DLMGYIPVV 140
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   ORIGINAL SOURCE:
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RESULT 13 US-08-290-665A-206

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Gaps
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APPLICANT: BUXH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMD THE USE OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STEEL: 345 PORGAN & FINNEGAN
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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88.9%; Pred. No. 0.45;
ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILLING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPRENCE/POCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-10398-178; Sequence 178, Application PC/TUS9510398; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 annho acids
TYPE: annho acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK2
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Best Local Similarity 88.3
Best Local Similarity 88.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW YORK
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF 1SOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%; Score 43; DB 4; Length 191; 88.9%; Pred. No. 0.45; ative 0; Mismatches 1; Indels
                          FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 759-4800
TELEFAX: (212) 759-4800
TELEFAX: (212) 759-6490
TELEFAX: (212) 759-6490
TELEFAX: (212) 759-6649
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GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
08/086,428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T9
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Matches 8; Conservative
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DLMGYIPAV 9
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APPLICANT: BURCHLL, R.H.
TITLE OF INVENTION: AND ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 4; Length 191;
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.5%; Scc. No. v. 88.9%; Pred. No. v. 0; Mismatches
                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
APPLICATION NUMBER: 08/290/665
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTONIEY, AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 179, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 751-6849
TELEX: 421792
INPORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: homosapiens
INDIVIDUAL ISOLATE: US10
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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 DLMGYIPVV 140
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Gaps

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PCT-US95-10398-182
Sequence 182, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AND AND DEDUCED
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
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                                          Score 43; DB 4; Length 191;
Pred. No. 0.45;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 4;
Pred. No. 0.45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA.
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION: 15-AUG-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
FRIOR APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 2026-4116
TELEPONE: (212) 758-4800
TELEPAX: (212) 758-4800
TELEFAX: (212) 758-480
TELEPAX: 421792
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.5%;
                                            91.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION NUMBER: PCT/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: US1
PCT-US95-10398-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 DLMGYIPUV 140
                                                                                                                                                                          132 DLMGYIPVV 140
                                                                                                                                  1 DLMGYIPAV 9
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STRANDEDNESS: un
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PCT-US95-10398-181
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NUCLEOTIDE AND DEDUCED
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                         Query Match
91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred, No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: 1BM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10398

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,428

FILING DATE: 15-AUG-1995

CLASSIFICATION NUMBER: 08/290/665

FILING DATE: 15 AUGUST 1994

APPLICATION NUMBER: 08/290/665

FILING DATE: 15 AUGUST 1994

ATTORNEY/AGENT INPORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4116

TELECOMMUNICATION INPREMATION:

TELECOMMUNICATION INPREMATION:

TELECOMMUNICATION INPREMATION:

TELECOMMUNICATION INPREMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 181, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BUKH, J., MILLER, R.H.
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MINO ACID SE
TITLE OF INVENTION: CORE GENES OF
TITLE OF INVENTION: CORE GENES OF
TITLE OF INVENTION: SEQUENCES IN
UNDER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STRIE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 181: SEQUENCE CHARACTERISTICS: LENGTH: 191 amino acids TYPE: amino acid STRANDEDNESS: unknown TOPOLOGY: unknown
                     TELEX: 421792
INPORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                  LENGTH: 191 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
CRIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T2
PCT-US95-10398-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
(212) 751-6849
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  TELEFAX:
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APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: ORDE GENES OF ISOLATES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 4; Length 191; Pred. No. 0.45;
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                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: BEA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORDERREGT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION NUMBER: 08/086,428
FILING DATE: 15-AUG-1995
CLASSIFICATION NUMBER: 08/290/665
FILING DATE: 15-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELEFONN: (212) 751-6849
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 751-6849
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 751-6849
TELEGRAY: (212) 751-6849
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NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative 0
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CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: homosapiens INDIVIDUAL ISOLATE: SW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
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                                                                                                                    R.H.
NUCLEOTIDE AND DEDUCED
NUCLEOTIDE AND DEDUCED
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY 1 USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION NUMBER: O8/086,428
FILING DATE: 29 JUNE 1993
APPLICATION NUMBER: 08/290/665
FILING DATE: 29 JUNE 1993
RPIOR APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTONNEY, AGENT INFORMATION:
NAME: RICHARD W. BORK
REDISTRATION NUMBER: 36,459
REPREDENCE/POCKET NUMBER: 36,459
REDISCAPIONE: (212) 758-4800
TELECHONE: (212) 758-4800
                                                                                                  MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MILLER, R.H. AND
                  PCT-US95-10398-183
; Sequence 183, Application PC/TUS9510398
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
PCT-US95-10398-184

; Sequence 184, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AN APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHRACTERISTICS:
LENGTH: 191 antho acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homosapiens
;
INDIVIDUAL ISOLATE: DK11
PCT-US95-10398-183
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORGAN & FINS
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                       APPLICANT: BUCH, J., MILIA APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLE TITLE OF INVENTION: CORE TITLE OF INVENTION: AND TITLE OF INVENTION: AND TITLE OF INVENTION: SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: unknown
unknown
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Matches 8, Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TOPOLOGY: unkr
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Gaps

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Query Match
91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCES/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 758-4800
FELER: 421792
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHRACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: WENDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION DATA:
PROBLICATION DATA:
PRICA APPLICATION DATA:
PRILING DATE: 29 JUNE 1993
FILING DATE: 19 JUNE 1994
APPLICATION NUMBER: 08/2065
FILING DATE: 15 AUGUST 1994
APPLICATION NUMBER: 36,459
RECASTRATION NUMBER: 36,459
RECASTRATION NUMBER: 36,459
RECASTRATION NUMBER: 36,459
RECASTRATION NUMBER: 36,459
RECECOMMUTCATION NUMBER: 30,759
RECECOMMUTCATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELESCOMMUTCATION INFORMATION:
TELESPHONE: (212) 758-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: $83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DLMGYIPAV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-10398-186
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NUCLEOTIDE AND DEDUCED
CORE GENES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
263
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88.9%; Pred. No. 0.45;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION:
TITLE OF INVENTION: CARE GENES OF ISOLAT;
TITLE OF INVENTION: CARE GENES OF ISOLAT;
TITLE OF INVENTION: AMINO ACID SEQUENCES;
TITLE OF INVENTION: SEQUENCES IN DIAGNOS
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: WORDBERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 29 JUNE 1994
APPLICATION NUMBER: 08/290/665
ATTORNEY/AGENT INFORMATION:
NAME: RIGHARD W. BORK
REGISTRATION NUMBER: 36,459
REPERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPERENCE MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: 1845 PARK AVENUE CITY: 1848 YORK STATE: NEW YORK STATE: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10154 FORD: 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 421792
INFORMATION FOR SEQ ID NO: 185: SEQUENCE CHARACTERISTICS: LENGTH: 191 amino acids TYPE: amino acid STRANBEDNESS: unknown TOPOLOGY: unknown ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homosapiens INDIVIDUAL ISOLATE: DK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.5
Best Local Similarity 88.9
Matches 8; Conservative
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Gaps

Gaps

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Sequence 203-2036

Sequence 203-403

Sequence 203-403

Sequence 203-403

Retent No. 6555114

GENERAL INFORMATION:
APPLICANT: LEROUX-ROLLS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: VINNO GOOTH
FILE REPERBNCE: 2752-18
CURRENT FALLING DATE: 1994-04-25
PRIOR PLING DATE: 1994-10-28
PRIOR PLING DATE: 1994-10-28
PRIOR PLING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTHARE: PATENTIN VERSION 3.1
SEQ ID NO 203
LENGTHREED
APPLICANT VERSION 3.1
SEQ ID NO 203
LENGTHREED
APPLICANT VERSION 3.1
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (66)...(66)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (5). (5)
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xea is any amino acid
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LOCATION: (95)...(95)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (193)...(193)
OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-203
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OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: hepatitis C virus
8; Conservative
                                                                                      132 DIMGYIPUV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE LOCATION: (5)...(5)
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                                           1 DLMGYIPAV 9
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                                                                                                                                                      RESULT 25
US-08-635-886C-203
  Matches
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                            Query Match 91.5%; Score 43; DB 4; Length 191; Best Local Similarity 88.9%; Pred. No. 0.45; Matches 8; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BUXH, J., MILLER, R.H. AND
APPLICANT: PUNCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUC
TITLE OF INVENTION: CORE GENES OF ISOLAT
TITLE OF INVENTION: CORE GENES OF ISOLAT
TITLE OF INVENTION: AND THE USE OF REAGE
TITLE OF INVENTION: SEQUENCES IN DIAGNOS
NUMBER OF SEQUENCES: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/29/665
FILING DATE: 15 AUGUST 1994
ATTOCNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 206, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO: 206: SEQUENCE CHARACTERISTICS: LENGTH: 191 anino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK STATE: STATE: STATE: NEW YORK STATE: NEW YORK COUNTRY: USA ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.5%;
                                                                                                    ORGANISM: homosapiens
i INDIVIDUAL ISOLATE: DK13
PCT-US95-10398-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPOLOGY: unknown ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homosapiens ; INDIVIDUAL ISOLATE: HK2 PCT-US95-10398-206
                TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & E
STREET: 345 PARK AVEN
                                                                                                                                                                                                                                                                                                                                     132 DLMGYIPVV 140
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Best Local Similarity
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Gaps

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Sequence 204, Application US/08974690C

| Sequence 204, Application US/08974690C
| Parent No. 6613333
| GENERAL INFORMATION:
| APPLICAMY: LEROUX-ROLE, Geert
| APPLICAMY: DELEYS, Robert
| APPLICAMY: INMUNITION: UNMUNITED INTERIOR OF HEPATITIS C
| TITLE OF INVENTION: UNFUS
| FILE REPERENCE: 2551-94
| CURRENT APPLICATION NUMBER: US/08/974,690C
| CURRENT APPLICATION NUMBER: PCT/EP94/03555
| PRIOR FILING DATE: 1997-11-19
| PRIOR FILING DATE: 1994-10-28
| PRIOR FILING DATE: 1994-10-48
| NUMBER OF SEQ ID NOS: 286
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 204
                                                US-UN-53-WEBC-204

Sequence 204, Application US/08635886C

Sequence 204, Application US/08635886C

SEXEMAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: URMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VINUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: PCT/EP94/03555
PRIOR PILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-48
PRIOR FILING DATE: 1993-11-04
NUMBER: O SEQ ID NOS: 286
SOSTWARR: Patentin version 3.1
SEQ ID NO 204
LIBRITAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2;
Pred. No. 0.77;
0; Mismatches
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88.9%; Pred. No. 0.77;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: hepatitis C virus US-08-974-690C-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 DLMGYIPVV 140
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 28
US-08-974-690C-204
                                              US-08-635-886C-204
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                                                                          RESULT 26
US-08-974-690C-203
i Sequence 203. Application US/08974690C
; Patent No. 661333
i GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNER: US/08/974,690C
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT FILING DATE: 1994-10-28
PRIOR PILING DATE: 1994-10-28
PRIOR PILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-3
TWHER OF SEQ ID NOS: 286
SOFTWARE: PATENTH OF SEQ ID NOS: 286
SOFTWARE: PATENTH OF SEQ ID NOS: 286
SEQ ID NO 203
TYPE: PRT
ORGANISM: hepatitis C virus
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88.9%; Pred. No. 0.46;
tive 0; Mismatches 1; Indels
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NAME/KEY: MISC_FEATURE

LOCATION: (193)..(193)

OTHER INFORMATION: Xea is any amino acid
US-08-974-690C-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (5). (5)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (18) .. (18)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE LOCATION: (119). (119). OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (173)..(173)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (58)...(58)
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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NAME/KEY: MISC_FEATURE
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6 DLMGYIPVV 14
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Best Local Similarity
Matches 8; Conserv
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RESULT 31
US-08-36-075A-44

| Sequence 44, Application US/08836075A
| Sequence 44, Application US/08836075A
| Sequence 44, Application US/08836075A
| Patent No. 618076
| GENERAL INFORMATION: GERT
| APPLICANT: STOTTER, LIEDEN
| ITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
| ITLE OF INVENTION: NEW SEQUENCES 207
| ITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
| TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
| TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
| TOWNESSER OF DIAGNOSTIC ADDRESS:
| ADDRESSER: ARMOLD, WHITE & DURKEE | STREET: P. O. BOX 4433 |
| CONPITS: READABLE FORM: | COMPATION: AND THEIR USE | CONPITS: IS P. O. BOX 4433 |
| CONPITS: READABLE FORM: | COMPATION: AND THEIR OF OF THE STREET: OF THE STREET
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Pred. No. 0.81;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION NUMBER: EP 95870076.7
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INPORMATION:
NAME: KAMMERER: PATTICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 29,775
REFERENCE CHARACTERISTICS:
LENGTH: 319 amino acide
TYPER: amino acide
TYPER: amino acide
TYPER: amino acide
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Best Local Similarity 88.5
Local Similarity 88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-18
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               PEPLICANT: MAERTENS, GERT
APPLICANT: MAERTENS, GERT
APPLICANT: MAERTENS, GERT
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 20.
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: P.O. BOX 4433
CITY: HOUSTON
STREET: P.O. BOX 4433
CITY: HOUSTON
STREET: P.O. BOX 4433
COUNTER: ELOROY disk
COUNTER: ELOROY disk
COMPUTER: ELOROY disk
COMPUTER: ELOROY disk
COMPUTER: IBM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: 1 APPLICATION DATA:
APPLICATION NUMBER: E PT[RPSS / 04155]
FILING DATE: 21 Apr 1997
PRIOR APPLICATION NUMBER: E PT[RPSS / 04155]
PRIOR APPLICATION NUMBER: E PT 1995
PRIOR APPLICATION NUMBER: E PS 94870166.9
PRIOR APPLICATION NUMBER: E PS 94870166.9
PRIOR APPLICATION NUMBER: E P 9487016.9
PROPRATION NUMBER: E P 9487016.9
PROPRATION POR SEQ ID NO: C. SEQ POR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08836075A

Patent No. 6180768

GENERAL INFORMATION:
APPLICANT: MAEKTENS, GERT
APPLICANT: STUTVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Pred. No. 0.81;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 318 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-836-075A-76
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       GENERAL INFORMATION:
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Gaps

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Gaps

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APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UMBUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UMBUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNBER: US/08/635,886C
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATCHIN VERSION 3:1
SEQ ID NO 2:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 228, Application US/08635886C

Batent No. 6555114

BATENT INFORMATION:
APPLICANT: DELEYS, Robert
APPLICANT: MARYENS, Geert
APPLICANT: MARYENS, Geert
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEBATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERRNCE: 2752-18
CURRENT PAPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
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Pred. No. 0.81;
0; Mismatches 1
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Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0, Mismatches
                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (131). (131) OTHER INFORMATION: Xaa is any amino acid PEATURE:
                                                                                                                                                                                                                  ; NAME/KEY: MISC_FEATURE
; LOCATION: (319)...(319)
; OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-635-886C-217
; Sequence 217, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
                                                                                                                                                                                                                                                                                                                              91.5%;
    NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 206
                                                                            TYPE: PRT
ORGANISM: hepatitis C virus
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-217
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.,
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Sequence 202, Application US/08635886C

Patent No. 655514

GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, Geert

APPLICANT: DELEXYS, Robert

APPLICANT: MAERTENS, Geert

APPLICANT: MAERTENS, Geert

TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2752-18

CURRENT APPLICATION NUMBER: US/08/635,886C

CURRENT APPLICATION NUMBER: EP94/03555

PRIOR FILING DATE: 1994-10-28

PRIOR FILING DATE: 1994-11-04

NUMBER OF SEQ ID NOS: 286

SEQ ID NO 202

LENGTH: 319

TYPE: BRT
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US-08-635-886C-206

i Sequence 206, Application US/08635886C

j Patent No. 6555114

i GENERAL INFORMATION:

APPLICANT: DELEVOK. POELS,

APPLICANT: DELEVS, Robert

APPLICANT: DELEVS, Robert

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2752-18

CURRENT FILING DATE: 1996-04-25

PRIOR PAPLICATION NUMBER: PCT/EP94/03555

PRIOR PLING DATE: 1994-10-28

PRIOR FILING DATE: 1993-11-04
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91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                Score 43; DB 2; Length 319;
Pred. No. 0.81;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (319)...(319)
OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-202
                           44:
                                                                                                                                                                                    91.5%;
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                           LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: hepatitis C virus
                                                                                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                               132 DLMGYIPVV 140
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US-08-635-886C-202
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Gaps

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MS-011.3

WS-08-974-690C-202

WS-08-974-690C-202

Sequence 202, Application US/08974690C

Patent No. 661333

GENERAL INFORMATION:

APPLICANT: LESTOUX-ROELS, Geert

APPLICANT: DELENS, Robert

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2551-94

CURRENT FILING DATE: 1997-11-19

PRIOR APPLICATION NUMBER: PP 93402718.6

PRIOR FILING DATE: 1994-10-28

PRIOR FILING DATE: 1994-10-28

PRIOR FILING DATE: 1994-11-04

NUMBER OF SEQ ID NOS: 286

SEQ ID NO 202

LENGTH: 319
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Batent No. 661333
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DELEYS, Robert
APPLICANT: MARKTENS, Geert
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REPERBNCE: 2551-94
CURRENT FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PCT/EP94/03555
                                                                                                                                                                                                                                                                                   Score 43; DB 2; Length 319;
Pred. No. 0.81;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                   1; Indels
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Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches
         LOCATION: (177)...(177)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
                                                                     NAME/KEY: MISC FEATURE COCATION: (232). (232) OTHER INFORMATION: Xaa is any amino acid PEATURE:
                                                                                                                                                                 NAME/KEY: MISC_FEATURE
COCATION: (233)...(233)
CTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-230
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NAME/KEY: MISC FEATURE
LOCATION: (3197)...(319)
US-08-974-690C-202
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Patent No. 655114

GENERAL INPORMATION:
PAPPLICANT: LEROUX-ROELS, Geert

APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMUNDER: US/08/635,886C

CURRENT APPLICATION NUMBER: PCT/EP94/03555

PRIOR APPLICATION NUMBER: EP 93402718.6

PRIOR FILING DATE: 1993-11-04

NUMBER: OF SEQ ID NOS: 286

SEQ ID NO 230

LENGTH: 319

LENGTH: 319
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Pred. No. 0.81;
0; Mismatches 1; Indels
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NAME/KEY: MISC FEATURE
LOCATION: (156)...(157)
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (167)...(167)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (171)...(172)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (161)...(161)
OTHER INFORMATION: Xaa is any amino acid
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 934
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 228
LENGTH: 319
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                          ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-228
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ORGANISM: hepatitis C virus
FEATURE:
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US-08-974-690C-217

Sequence 217, Application US/08974690C

Betent No. 661333

GENERAL INFORMATION:
APPLICANT: LEROUX-ROLES, Geert
APPLICANT: DELENGY, ROLES,
TITLE OF INVENTION: INMUNOCOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: INMUNOCOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94

CURRENT APPLICATION NUMBER: US/08/974,690C

CURRENT PAPLICATION NUMBER: PCT/EP94/03555
PRIOR PILING DATE: 1997-11-19

PRIOR PILING DATE: 1997-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 217

LENGTH: 319

TYPE: PATENTIAL OF THE OFFICE OF
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Sequence 228, Application US/08974690C

Sequence 228, Application US/08974690C

Sequence 228, Application US/08974690C

PAPALICANT: OFISSA33

APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

APPLICANT: MAERTENS, Geert

TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEFATITIS C

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2551-94
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Pred. No. 0.81;
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91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels
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LOCATION: (131)...(131)

OTHER INFORMATION: Xaa is any amino acid

FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (319)...(319)

OTHER INFORMATION: Xaa is any amino acid
US-08-974-690C-206
PRIOR FILING DATE: 1994-10-28
PRIOR PAPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 206
LENGTH: 319
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Best Local Similarity 88.9%;
Matches 8; Conservative
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; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
PRIOR PELING DATE: 1994-10-28
; PRIOR PELING DATE: 1994-10-28
; PRIOR FILING DATE: 1994-10-28
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOTWARE: Patentin version 3.1
; SEQ ID NO 228
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-228

Query Match
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps

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Db 132 DLMGXIPAV 140

Search completed: January 20, 2006, 22:42:33
Job time: 24 secs
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Sequence 5
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US-10-793-626-174
US-10-873-528-114
US-11-055-822-536
   11196
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   Sequence 211, App
Sequence 3, Appli
Sequence 2474, Ap
Sequence 55, Appl
Sequence 7774, Ap
Sequence 12, Appl
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                                                                                                           January 20, 2006, 22:42:04; Search time 30 Seconds (without alignments) 3.040 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
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              GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-985-205-3

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US-10-86-501-12

US-10-12-144-12

US-10-986-501-12

US-10-986-501-156

US-11-055-822-156

US-11-055-822-154

US-11-055-822-154

US-11-055-822-154

US-11-055-822-154

US-11-055-822-154

US-11-055-822-1154

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US-11-019-711-108
US-10-467-657-4026
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Maximum Match 100%
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Matches 6; Conser
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Publication No. US2005266400A1

GENERAL INFORMATION:
APPLICANT: Dumonceaux, Julie
APPLICANT: Dumonceaux, Julie
APPLICANT: Dandic, Tatjana
TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS
FILE REFERENCE: 71242-A/JPW/AJD
CURRENT APPLICATION NUMBER: US/10/985,205
CURRENT APPLICATION NUMBER: US 60/519,536
FILE REPERENCE: 2003-11-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 3
LUMBER OF SEQ ID NOS: 20
SEQ ID NO 3
LUMBER OF SEQ ID NOS: 20
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Sequence 75, Appl
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US-11-02-562-211
Sequence 211, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: RUDIECHL, Ruth M.
APPLICANT: Shisong, Jiang
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
ITILE OF INVENTION: ACTOTOXIC T LYMPHOCYTE INMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR FILING DATE: 2004-12-22
PRIOR PILING DATE: 2003-06-27
PRIOR PILING DATE: 2003-06-27
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 211
LENGTH: 2280
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Pred. No. 1.8;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 7; Length 2280;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
US-11-055-822-630
US-10-995-793-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.4%;
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۰ 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-11-022-562-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
300
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55.3
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26
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Sequence 2474, Application US/10467657

Publication No. US20050260581A1

GENERAL INCORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNAI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REPERENCE:

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQ ID NOS: 9218

SEQ ID NO SEQ ID NOS: 9218

SEQ ID NO SEQ ID NOS: 9714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 6; Length 777;
Pred. No. 11;
0; Mismatches 1; Indels
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gequence 55, Application US/10873528

publication No. US20050276814A1

GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Microbial Technics Limited
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: US 6991769,787
PRIOR FILLING DATE: 1998-03-27
PRIOR FILLING DATE: 1998-03-27
PRIOR FILLING DATE: 1998-03-19
FRIOR FILLING DATE: LDSGREEN US 60/125164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7774, Application US/10467657; Publication to US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae US-10-873-528-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2474
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Best Local Similarity 87.5
Matches 7; Conservative
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Gaps
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NUMBER OF SEQ ID NOS: 373
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 169
LENGTH: 103
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Pred. No. 45;
1; Mismatches 1; Indels
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| US-10-986-501-169|
| US-10-986-501-169|
| US-10-986-501-169|
| Sequence 169, Application US/10986501
| Publication No. US20050244845A1
| GENERAL INPORMATION:
| APPLICATION OF Human Secreted Proteins FILE REFERENCE: P2013P201
| CURRENT PAPLICATION NUMBER: US/10/986,501
| CURRENT PAPLICATION NUMBER: US/10/621,363|
| PRIOR APPLICATION NUMBER: 09/969,730|
| PRIOR PILING DATE: 2001-10-06|
| PRIOR PILING DATE: 2001-00-06|
| PRIOR PILING DATE: 2001-00-06|
| PRIOR PILING DATE: 2000-10-06|
| PRIOR PILING DATE: 2000-10-06|
| PRIOR PILING DATE: 1999-02-04|
| PRIOR PILING DATE: 1999-02-04|
| PRIOR PILING DATE: 1999-03-04|
| PRIOR PILING DATE: 1999-03-04|
| PRIOR PILING DATE: 1997-08-19|
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                  RADESTRATION NUMBER: 37,003
RADESTRATION NUMBER: 37,003
REPERRENGE/DOCKET NUMBER: 5D9951IA
TELECOMMUNICATION INPORMATION:
TELEPHONE: 732-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acids
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.8%; Score 30; DB 71.4%; Pred. No. 12; :ive 1; Mismatches
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5, Conservative
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US-10-986-501-169
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US-11-122-144-12

Sequence 12, Application US/11122144

Sequence 12, Application No. US20050287663A1

Publication No. US20050287663A1

GENERAL INFORMATION:

APPLICANT: Gillespie, Alison

Claeps, Brian O.

Chavez-Noriega, Laura Blena

Siegel, Robert

Billott, Kathryn J.

TITLE OF INVENTION: DNA ENCODING HUMAN ( AND ( SUBUNITS )

RECEPTOR, CELLS TRANSFORMED THEREWITH,

AND RECOMBINANT CELL LINE EXPRESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
             APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
TITLE ON INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9216
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 7774
LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: USA
ZIALE: NO.
COUNTY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/11/122,144
FILING DATE: 01-NOV-2000
APPLICATION NUMBER: US/09/703,951
FILING DATE: 08-MAR-1994
APPLICATION NUMBER: US 08/449,503
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 09/938,154
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/504,455
FILING DATE: ADDITION NUMBER: US 07/504,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.0%; Score 31; DB 6; Length 415; Best Local Similarity 71.4%; Pred. No. 36; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-APR-1990
                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7774
APPLICANT: FONTANA Maria Rita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rahway
STATE: NJ
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103 DIIGYİEAM 111
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26 GYLPAV 31
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                  US-11-055-822-156
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RESULT 8
US-10-793-626-1446
is Sequence 1446, Application US/10793626
is Sequence 1446, Application US/10793626
is Publication No. US20050255478A1
is GENERAL INFORMATION:
is TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
is FILE REFERENCE: PU3480US
is CURRENT FILING DATE: 1090-10-09
is PRIOR FILING DATE: 1999-11-09
is NUMBER OF SEQ ID NOS: 4472
is SOFTWARE: Patentin Ver. 2.1
is SEQ ID NO 1446
is LENGTH: 121
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NUMBER OF SEQ ID NOS: 1158
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Sequence 156, Application US/11055822

PUBLICANT: Pompejus, Markus

APPLICANT: Pompejus, Markus

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Aberhauer, Gregor

TITLE OF INVENTION: CRYNEBACTERIUM GENES ENCODING

TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

TITLE OF INVENTION: WETABOLIC PATHWAY PROTEINS

FRICH FILING DATE: 1090-06-23

PRIOR FILING DATE: 1099-06-25

PRIOR PILING DATE: 1099-06-25

PRIOR FILING DATE: 1099-07-02

PRIOR FILING DATE: 1099-07-02

PRIOR FILING DATE: 1099-07-08

PRIOR PILING DATE: 1099-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LIGYIPFI 37
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                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU348002
CURRENT PRILING DATE: 2004-03-04
PRIOR PPLICATION NUMBER: 06/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTHARE: Patentin Ver. 2.1
ENGTH, 146
                                              Gaps
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
is OTHER INFORMATION: amino acid sequence
15-10-793-626-802
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Sequence 16, Application US/11075185

PUBLICARIN NO. US20850266434A1

GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
APPLICANT: RID, RALPH

TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REFERENCE: 010099.03

CURRENT APPLICATION NUMBER: US/11/075,185

CURRENT PILING DATE: 2005-03-08

PRIOR PELIOR OF SEQ 10 NOS: 61

NUMBER OF SEQ 1D NOS: 61

SOFTWARE: Patentin version 3.3

SEQ 1D NO 16

LENGTH: 356
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Score 30; DB 7; Length 130;
Pred. No. 15;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                        Sequence 802, Application US/10793626; Publication No. US20050255478A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Sorangium cellulosum US-11-075-185-16
    63.8%;
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 83.3
Matches 5, Conservative
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62;
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Sequence 5282, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON Spa
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.8%; Score 30; DB
83.3%; Pred. No. 62;
tive 1; Mismatches
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum
US-11-055-822-154
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Best Local Similarity 83.3
Matches 5; Conservative
121 DAEGYVPA 128
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26 GYLPAV 31
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Sequence 4228

Publication No. US2005260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTAAN MATIA Rita

APPLICANT: FONTAAN MATIA RITA

APPLICANT: PIZZA MATIAGRAZIA

APPLICANT: MASSIGNANI Vega

APPLICANT: MASSIGNANI Vega

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT PILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2010-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWing9, version 1.04

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Publication No. U320050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rica
APPLICANT: PONTANA Maria Rica
APPLICANT: PASE Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                              Score 29; DB 6;
Pred. No. 14;
2; Mismatches
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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                                                                    ; TVPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 6612
LENGTH: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Neisseria gonorrhoeae
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-467-657-6612
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SEQ ID NO 5282
LENGTH: 80
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US-11-US-822-308

Sequence 308, Application US/11055822

Publication No. US20050260707A1

GENERAL INFORMATION

APPLICANT: Pompedus, Markus

APPLICANT: Schroder, Hartwig

APPLICANT: ABDERHAUS: GENERAL

APPLICANT: ABDERHAUS: GENERAL

TITLE OF INVENTION: CORYNEBACTERIUM GENTES ENCODING

TITLE OF INVENTION: WETABACTERIUM GENES ENCODING

TITLE OF INVENTION: WETABACTERIUM GENES ENCODING

TITLE OF INVENTION: WETABACTERIUM GENER (6/14)

PRICH PRICH APPLICATION NUMBER: 06/141,031

PRICH PLING DATE: 1999-06-25

PRICH PLING DATE: 1999-06-25

PRICH PLING DATE: 1999-06-25

PRICH PLING DATE: 1999-06-25

PRICH PLING DATE: 1999-06-26

PRICH PLING DATE: 1999-07-01

PRICH PLING DATE: 1999-07-06

PRICH PLI
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
NUMBER: OF SEQ ID NOS: 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: 183
COTHER INFORMATION: Xaa = Phe, Leu, Ile, or Val
US-11-055-822-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT

OGGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: VARIANT
LOCATION: (181)...(182)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
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Best Local Similarity 55.6
Matches 5; Conservative
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                                      Gaps
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Sequence 312, Application US/11055822

Sequence 312, Application US/11055822

Publication No. US20050260707A1

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Calder, Oskar
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION WUMBER: US/11/05,822
CURRENT FILING DATE: 2006-02-11
FRIOR APPLICATION NUMBER: 60/141,031
FRIOR FILING DATE: 1999-06-25
FRIOR FILING DATE: 1999-08-12
FRIOR APPLICATION NUMBER: 60/146,613
FRIOR APPLICATION NUMBER: 60/146,613
FRIOR FILING DATE: 2000-03-09
FRIOR FILING DATE: 2000-03-09
FRIOR FILING DATE: 2000-03-09
FRIOR FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                           RESULT 16

US-11-188-743-15

i Sequence 15, Application US/11188743

i Publication No. US20050272140A1

i GENERAL INFORMATION:

APPLICANT: Sias, Philip

APPLICANT: Kinzler, Kenneth

APPLICANT: Grasso, Luigi

APPLICANT: Vogelstein, Bert

ITLE OF INVENTION: Methods for generating hypermutable

TILE REPERENCE: 01107.00097

ITLE REPERENCE: 01107.00097

CURRENT APPLICATION NUMBER: US/11/188,743

CURRENT FILING DATE: 2005-07-26

PRIOR PILICATION NUMBER: US/10/641,068

PRIOR PILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PASESEQ for Windows Version 3.0

SEQ ID NO 15
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-188-743-15
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Best Local Similarity 62,5%;
Matches 5; Conservative
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1; Indels

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US-11-010-874-7

Sequence 7, Application US/11010874

Publication No. US2055256694A1

Publication No. US2055256694A1

JEDRICANT: Ma. US2055256694A1

APPLICANT: Ma. Jian-Xing

TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAWMATION A

TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME

FILE REFERENCE: 5820.656

CURRENT APPLICATION NUMBER: US/11/010,874

CURRENT PILLING DATE: 2004-12-13

PRIOR FILLING DATE: 2004-10-12

PRIOR FILLING DATE: 2003-10-10

PRIOR FILLING DATE: 2003-12-11

PRIOR FILLING DATE: 2003-12-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Version 3.3

SEQ ID NO 70
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Publication No. US20050246784A1

GENERAL INFORMATION:

APPLICANT: Plesch, Gunnar

APPLICANT: Blau, Astrid

APPLICANT: Daeschner, Klaus

APPLICANT: Mathiau

TITLE OF INVENTION: Identification of Herbicidally Active Substances

TITLE REFERENCE: 2000 857

CURRENT APPLICATION NUMBER: US/10/467,962B

CURRENT APPLICATION NUMBER: PCT/EP02/01466

PRIOR APPLICATION NUMBER: PCT/EP02/01466

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 109

SOFTWARE: Patentin Vers. 2.0

LENGTH: 257
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US-10-467-962B-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.6
Best Local Similarity 100.
Matches 5; Conservative
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153 DLVGYI 158
                                                                116 GYIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIMGYI 6
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                          4 GYIPA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GYIPA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: murine US-11-010-874-7
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US-10-467-962B-73
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Sequence 12, Application US/11010874

Sequence 12, Application US/11010874

Sequence 12, Application US/11010874

Sequence 12, Application US/11010874

Sequence 12, Application No. US20050250694A1

SETILE TO TIVEWATION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND TITLE OF INVENTION: FIRENCE: 5020.656

CURRENT APPLICATION NUMBER: US/11/010, 874

CURRENT PILING DATE: 2004-12-13

PRIOR PLILNG DATE: 2004-10-12

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-10

SPRIOR APPLICATION NUMBER: 60/510,620

PRIOR FILING DATE: 2003-12-11

NUMBER OF SEQ ID NOS: 18

SSOUTH NOS: 18

LENGTH: 160

LENGTH: 160
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                                                           Query Match 61.7%; Score 29; DB 7; Length 1152; Best Local Similarity 55.6%; Pred. No. 3.1e+02; Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      Sequence 2492, Application US/10467657

Sequence 2492, Application US/10467657

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: POUTANA Maria Rita
APPLICANT: POUTANA Maria Rita
APPLICANT: MASIGNAIN VGBA

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT APPLICATION NUMBER: GB-0103424.8

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR PILLING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQ ID NOS: 9218

SEQ ID NO 2492

LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 6; Length 128;
Pred. No. 40;
4; Mismatches 0; Indels
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51;
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; ORGANISM: Corynebacterium glutamicum
US-11-055-822-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.9'
Matches 3, Conservative
                                                                                                                                                                             :|:|:|||
390 ELLLYVPAV 398
                                                                                                                                                     1 DLMGYIPAV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |::|::|
63 DIIGEVP 69
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ORGANISM: murine
                                                                                                                                                                                                                                                                                       US-10-467-657-2492
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Sequence 4026, Application US/10467657

Publication No. US20050260581A1

GENERAL INPORMATION:

APPLICANT: FOUTANA Maria Rita
APPLICANT: FOUTANA Maria Rita
APPLICANT: FOUTANA Maria Rita
APPLICANT: MASIGNANI Vega
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT APLICATION NUMBER: 2003-08-11
PRIOR APPLICATION NUMBER: 2001-02-12
NUMBER: OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4026
LENGTH: 332
                                                                                                   Anderson, David W
Padigaru, Muralidhara
Taupier Jr, Raymond J
Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4026
                                Ferenc L
                                                                       Shenoy, Suresh G
                                Boldog, Fere
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
) ORGANISM: Homo sapiens
US-11-019-711-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: ||:||
26 EIPGYLPA 33
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NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 314
LENGTH: 268
TYPE: PRT
US-11-055-822-314

; Sequence 314, Application US/11055822
; Publication No. US20050260707a1
; Publication No. US20050260707a1
; GENERAL INFORMATION:
; APPLICANT: Pompedus, Markus
; APPLICANT: Schoder, Harvad
; APPLICANT: Schoder, Harvad
; APPLICANT: Alberhauer, Gener
; TITLE OF INVENTION: ORNUBBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REPRENCE: BGI-121CPAT
; CURRENT APPLICATION HUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.6%; Score 28; DB 7; Length 268; 66.7%; Pred. No. 93; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR PILING DATE: 2000-06-23
PRIOR PELICATION NUMBER: 60/141,031
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 2000-03-09
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-06
PRIOR PELING DATE: 1999-07-06
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PRIOR PELING DATE: 1999-07-06
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US-11-055-822-314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alsobrook II, John P
Tchernev, Velizar T
Liu, Xiaohong
Spytek, Kimberly A
Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Vernet, Corine A.M.
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Edinger, Shlomit R
Sciore, Paul
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Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothenberg, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kekuda, Ramesh
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APPLICANT:
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APPLICANT:
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Gaps
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0
APPLICANT: Miller, Charles E
APPLICANT: Bisen, Andrew J
TITLE OF INVENTION Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR PELIOR FILING DATE: 2004-01-05
PRIOR PELIOR PRESENCE: 80/260,018
PRIOR PELIOR OFFE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR APPLICATION NUMBER: 60/220,411
PRIOR PELING DATE: 2001-02-29
PRIOR PILING DATE: 2001-02-29
PRIOR PILING DATE: 2001-03-02
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR PILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR PILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-07-05
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PRIOR PILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-09-12
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59.6%; Score 28; DB 7; Length 312
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels
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Gaps
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                                                                                                                                                                           Sequence 8252, Application US/10467657
; Sequence 8252, Application US/10467657
; Publication No. US2005026051A1
; GENERAL INPORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANN Maxia Rita
APPLICANT: FONTANN Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT APPLICATION NUMBER: GB-0103424.8
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8252
; LENGTHRES SeqWin99, version 1.04
; SEQ ID NO 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence; Note OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 28; DB 7; Length 550; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 411,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.6%; Score 28; DB 6; Length 411
80.0%; Pred. No. 1.5e+02;
tive 1; Mismatches 0; Indels
  Indels
  5
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/11184380
Publication No. US20050255089A1
GENERAL INFORMATION:
APPLICANT: Chiorini, John
APPLICANT: Chiorini, John
TITLE OF INVENTION: AAVS NUCLEIC ACIDS
FILE REFERENCE: 14014.0333U3
CURRENT APPLICATION NUMBER: US/11/184,380
CURRENT FILING DATE: 2005-07-19
FRIOR PILING DATE: 1999-05-28
FRIOR APPLICATION NUMBER: 60/087,029
FRIOR FILING DATE: 1998-05-28
FRIOR FILING DATE: 1998-05-28
FRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 80.0.
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  5; Conservative
                                                                                   46 ELGGYLPBV 54
                                         1 DLMGYIPAV 9
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                                                                                                                                                  RESULT 28
US-10-467-657-8252
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LENGTH: 550
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  Matches
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                                                                                                                                                                                                                                                   Sequence 2, Application US/11010874

Publication No. US20050250694A1

GENERAL INFORMATION

TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND

TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME

FILE REFERENCE: 5820.65

CURRENT PILING DATE: 2004-12-13

PRIOR PILING DATE: 2004-10-12

PRIOR APPLICATION NUMBER: 60/510,620

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-12-11

NUMBER OF SEQ ID NOS: 18

SSOFTARE: Patentin version 3.3

LENGTH: 339
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Sequence 28, Application US/10525674

Sebatal INFORMATION:

APPLICANT: Kroger, Burkhard

APPLICANT: Zelder, Oskar

APPLICANT: Acipproges, Corinna

APPLICANT: Schroder, Hartwig

APPLICANT: Hafner, Stefan

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals

CURRENT APPLICANT: Sulphur (Meta)

FILE REFERENCE: 1311-00002-US

CURRENT APPLICATION NUMBER: US/10/525,674

CURRENT PILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: PCT/EP 2003/009452

PRIOR PILING DATE: 2003-08-26

PRIOR PILING DATE: 2003-08-26

NUMBER OF SEQ ID NOS: 69

SEQ ID NOS: 69

SEQ ID NOS: 69

LENGTH: 380
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             Query Match 59.6%; Score 28; DB 6; Length 332; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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1.2e+02;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.6%; Score 28; DB 100.0%; Pred. No. 1.2; ive 0; Mismatches
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US-10-525-674-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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                                                                                                                                      79 GYIPA 83
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/ ORGANISM: murine
US-11-010-874-2
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US-11-010-874-2
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APPLICANT: Frey, Bruno
APPLICANT: Antranikian, Garabed
APPLICANT: Boehlke, Kristina
APPLICANT: Boehlke, Kristina
APPLICANT: Boehlke, Kristina
APPLICANT: Rossi, Mose
TITLE OF INVENTION: Mutant B-type DNA Polymerases Exhibiting Improved Performance i
FILE REFERENCE: 5238
CURRENT PILING DATE: 2005-03-11
FRICA APPLICATION NUMBER: US/09/803,165
PRICA FILING DATE: 2001-03-09
PRICA FILING DATE: 2000-03-11
PRICA FILING DATE: 2000-03-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 774
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Sequence 1, Application US/10795201

Sequence 1, Application WOS (10795201)

Publication No. US20050282171A1

GENERAL INFORMATION:

APPLICATION WATHION: PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA

TITLE OF INVENTION: POLYMERASE I

FILE REFERENCE: 4121.0004-06

CURRENT APPLICATION NUMBER: US/10/795,201

CURRENT PILING DATE: 2002-06-19

FRIOR APPLICATION NUMBER: US 09/244,889

FRIOR FILING DATE: 1999-02-05

FRIOR PILING DATE: 1991-02-05

FRIOR PILING DATE: 1991-02-05

FRIOR PILING DATE: 1991-02-05

FRIOR PILING DATE: 1991-02-15

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1991-02-19

FRIOR PILING DATE: 1990-12-03

NUMBER OF SEQ ID NOS: 6

SOGTHARRE: PATENTIN VETRION 3.1
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LENGTH: 775

TYPE: PRT

CRGANISM: Pyrococcus furiosus

US-10-795-201-1
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Best Local Similarity 44.*.
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                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: T. aggregans
US-11-077-886-34
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US-10-467-657-6470
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                                                                                                                                                                                 APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: 105/0/770,726
CURRENT APPLICATION NUMBER: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 603
LENGTH: 603
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US-11-184-380-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.6%; Score 28; DB 7; Length 610; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.6%; Score 28; DB 6; Length 603; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COSTILIBATION OF USCULIA SEQUENCE 3, Application US/11184380 SEQUENCE 3, Application US/11184380 SEQUENCE 3, Application No. US200502508911 GENERAL INFORMATION: APPLICANT: Chiorini, John TITLE OF INVENTION: AAV5 NUCLEIC ACIDS FILE REFERENCE: 14014.032313 CURRENT APPLICATION NUMBER: US/11/184,380 CURRENT PILING DATE: 2005-07-19 PRIOR PILING DATE: 1999-05-28 PRIOR PILING DATE: 1999-05-28 PRIOR PILING DATE: 1999-05-28 NUMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 610
                                                RESULT 30
US-10-770-726-75
Sequence 75, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 34, Application US/11077886; Publication No. US20050266436A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Homo sapiens

US-10-770-726-75
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US-11-077-886-34
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US-11-184-380-3
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Sequence 70, Application US/11102240

Sequence 70, Application US/11102240

Sublication No. US20050260647A1

GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BSOPHAGEAL TUMOR
FILE REFERENCE: P3230ALC106C

CURRENT APPLICATION NUMBER: US/11/102,240

CURRENT APPLICATION NUMBER: 10/063662
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APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Mary E.
APPLICANT: Gerritean, Mary E.
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Grimald, Christopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wonger: US/10/063, 703
CURRENT FILING DATE: 2002-05-08
PRIOT APPLICATION TOWNER: Marapper
NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                59.6%; Score 28; DB 6; Le 100.0%; Pred. No. 3.8e+02; iive 0; Mismatches 0;
           CURRENT APPLICATION NUMBER: US/10/967,648A CURRENT FILING DATE: 2004-10-15 PRIOR APPLICATION NUMBER: USSN 60/512010 PRIOR FILING DATE: 2003-10-16 NUMBER OF SEQ ID NOS: 16 SOFTWARE: Patentin version 3.3 SEQ ID NO 14 LENGTH: 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-063-703-70
; Sequence 70, Application US/10063703
; Publication No. US20060008901A1
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Best Local Similarity 50.0%;
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Best Local Similarity 100.
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618 LQGYVPVL 625
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; ORGANISM: Homo Sapien
US-10-063-703-70
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                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                         US-10-967-648A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ## APPLICANT: Ma. Jan.Xing
## APPLICANT: Ma. Jan.Xing
## TITLE OF INVENTION: COMPOUNDS USEPUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
## TITLE OF INVENTION: COMPOUNDS USEPUL IN INHIBITING SAME
## TITLE OF INVENTION: FIRENOSIS AND METHODS OF MAKING AND USING SAME
## FILENOSIS SAD. 656
## CURRENT PAPLICATION NUMBER: US/11/010,874
## CURRENT FILING DATE: 2004-12-13
## PRIOR PILING DATE: 2004-10-10
## PRIOR PILING DATE: 2003-10-10
## PRIOR PILING DATE: 2003-10-10
## PRIOR PILING DATE: 2003-12-11
## NUMBER OF SEQ ID NOS: 18
## SOFTWARE: PATENTIN VERSION 3.3
## SEQ ID NO 1
## LENGTH: 812
## CORGANISM: murine
## US-11-010-874-1
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10-87-648A-14
18-10-967-648A-14
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18-10-967-648A-14
18-10-968-14
19-10-968-14
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GENERAL INFORMATION:
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APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: POTZAM Mariagrazia
APPLICANT: MASIGNANI Voga
APPLICANT: MASIGNANI Voga
APPLICANT: MONACI Elisabetta
TITLE OF INVERTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENT SPAPLICANTON NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR RILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOUTHARE: SeqWin99, version 1.04
SEQ ID NO 6470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.6%; Score 28; DB 6; Length 801; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6470
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Matches 5; Conservative
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Fublication No. US20050288866A1

GENERAL INFORMATION:
FUBLICANTION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATION OF THERAPEUTIC POTENTIAL
FILE OF INVENTIONAL METHOD OF THE 2005-02-07
FRIOR APPLICATION NUMBER: US 60/589,227
FRIOR PILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
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Sequence 72, Application US/10858730

FUBLICANT: Bailey, Richard B.

APPLICANT: Bailey, Richard B.

APPLICANT: Bolomquist, Paul

APPLICANT: Doten, Reed

APPLICANT: O'Leary, Jesaica

APPLICANT: O'Leary, Jesaica

APPLICANT: Walbridge, Michael J.

APPLICANT: Walbridge, Michael J.

APPLICANT: Yorgey, Peter S.

TITLE OF INVENTION: MEROUUTION

FILE REFERENCE: 14184-030001
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ilarity 44.4%; Pred. No. 4.3e+02;
Conservative 3; Mismatches 2;
ORGANISM: Haemophilus influenzae Rd
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Best Local Similarity 50.0
Matches 4; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen I	protein search, using sw model	January 20, 2006, 22:24:52; Search t (without a 90.711 Mill Mill	US-10-770-117-1 :e: 47 1 DIMGYIPAV 9	e: BLOSUM62 Gapop 10.0 , Gapext 0.5	2166443 seqs, 705528306 residues	of hits satisfying chosen parameters:	eq length: 0 eq length: 200000000	ssing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	<pre>UniProt_05.80:* 1: uniprot_sprot:* 2: uniprot_trembl:*</pre>	No. is the number of results predicted greater than or equal to the score of t derived by analysis of the total score	SUMMARIES	OΣ	91.5 136 2	43 91.5 137 2 Q7TLG1 9HEPC 43 91.5 137 2 Q7TLG2 9HEPC 137 2 Q7TLG3 9HEPC	91.5 137 2 91.5 137 2	91.5 137 2 91.5 137 2	91.5 137 2 91.5 167 2	91.5 188 2 91.5 191 2	91.5 191 2 91.5 191 2	91.5 191 2 91.5 191 2	91.5 191 2	91.5 191 2	91.5 191 2	91.5 191 2	91.5 191 2	91.5 192 2	91.5 195 2 91.5 235 2	91.5 235 2 068694
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Matches 8; Conservative
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Hepatitis C virus.
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                    99 DLMGYIPVV 107
1 DLMGYIPAV 9
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                     Hepacivirus
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MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

T wingue pattern of endemic infection in Cameroon.";

L Gen. Vir.0. 184:333-2341(2003).

EMBL; AY256806; AAP34670.1; -; Genomic_RNA.

GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

InterPro; IPR002522; HCV_core.

InterPro; IPR002521; HCV_core.

R Pfam; PF01543; HCV_core.

R Pfam; PF01542; HCV_core; I.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
Core protein (Fragment)
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                      Viruses, ssRNA positive-strand viruses, no DNA stage, Flaviviridae, Hepacivirus.
                                                                                                                                          MUCLEOTIDE SEQUENCE.

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

A NGJomou J. Pybus O.G., Matz B.;

NGJomou J., Pybus O.G., Matz B.;

"Phylogenetic analysis of hepatitis C virus isolates indicates a

I unique pattern of endemic infection in Cameroon.";

J. Gen. Virol. 84,2333-2341(2003).

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R InterPro; IPR00252; HCV_capsid.

R InterPro; IPR002521; HCV_capsid.

R Pfam; PF01543; HCV_capsid; 1.

R Pfam; PF01542; HCV_core; 1.
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NON TER 136 136
SEQUENCE 136 AA; 14878 MW; B3FB67DDFF37DC0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 137 AA; 14992 MW; 6BD2F278178C5F4D CRC64;
              OTILES 9HEPC PRELIMINARY; PRT; 136 AA. Q7TLES, 01-0CT-2003 (TYENBLrel. 25, Created) 01-0CT-2003 (TYENBLrel. 25, Last sequence update) 01-MAR-2004 (TYENBLYEL). 26, Last annotation update) Core protein (Fragment).
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Best Local Similarity 88.9°
Matches 8; Conservative
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                                                                                                                       NCBI_TaxID=11103;
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MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

I window Jacken of Good of Marza Backerian in Cameroon.";

J. Gen. Virol. 84:2333-2341(2003).

E MEMBL; AZ256804; AAP34668.1; -; Genomic_RNA.

GO; GO:0019028; C:viral capaid; IEA.

GO; GO:0019028; C:viral capaid; IEA.

GO; GO:0015908; F:structural molecule activity; IEA.

R InterPro; IPR002521; HCV_capaid; I.

R Pfam; PF01543; HCV_capaid; I.

MANN map PF01542; HCV_cape: 1.
                                                                                                                                                                                                                                                                                                                   Core protein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepacivirus.
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A MEDLINE-22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
A McJomou J., Pybus O.G., Matz B.;
A McJomou J., Pybus O.G., Matz B.;
T whylogenetic analysis of hepatitis C virus isolates indicates a nunque pattern of endemic infection in Cameroon.";
J. Gen. Virol. 84:2333-2341(2003).
R EMBL; AY25805; AAP34669.1; -; Genomic_RNA.
GO; GO:0019028; C:viral capsid. IEA.
GO; GO:0019028; C:viral capsid. IEA.
R InterPro; IPR002522; HCV_capsid.
R InterPro; IPR002521; HCV_core.
R Pfam; PF01543; HCV_core; J.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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QTLG3;
QTLG3;
QTLG3 (TEMBLrel. 25, Created)
01-OCT-2003 (TEMBLrel. 25, Last sequence update)
01-OCT-2003 (TEMBLrel. 26, Last annotation update)
137 AA
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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NUCLEOTIDE SEQUENCE.

X MEDLINE-22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

X MEDLINE-22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

X MADLINE-22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;

XI Midjomou J., Pybus O.G., Matz B.;

XI Unique pattern of endemic Infection in Cameroon.";

XI Unique pattern of endemic Infection in Cameroon.";

XI J. Gen. Virol. 84:233-3241(2003).

B MBD; AYS56801; AAP34665-1; -; Genomic_RNA.

BR GO; GO:0019028; C:viral capsid; IEA.

BR GO; GO:0005198; F:setructural molecule activity; IEA.

BR InterPro; IPR002521; HCV_capsid.

BR InterPro; IPR002521; HCV_capsid.

BR InterPro; PF01543; HCV_capsid.

BR Pfam; PF01543; HCV_capsid.

BR Pfam; PF01542; HCV_capsid.
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                                                                                                                                                                                          Length 137;
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137 AA; 15000 MW; D17F9B2D8C78F647 CRC64;
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137 AA; 14890 MW; GBD8373BF43909B8 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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88.9%; Pred. No. 3;
tive 0; Mismatches
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88.9%; Pred. No. 3;
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  InterPro; IPR002521; HCV core
Pfam; PF01543; HCV caps1d; 1.
Pfam; PF01542; HCV core; 1.
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Q7TLG7 9HEPC PRELIMINARY;
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Hepatitis C virus.
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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Hepacivirus.
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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R Gen. Virol. 84:233-2341(2003).

R GO; GO:0019028; C:viral capsid; IGEN.

R GO; GO:0005198; F:structural molecule activity; IEA.

R InterPro; IPR00252; HCV capsid; R InterPro; IPR002521; HCV capsid.

R Ffam; PF01543; HCV_core: 1.

R Pfam; PF01542; HCV_core: 1.
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EMBL, AX256802; AAP34666.1; -; Genomic_RNA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR002522; HCV_capsid.
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MEDLINE=9322486; PubMed=8385694;
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Simmonds P., McOmlah F., Yap P.L., Chan S.-W.W., Lin C.K.,
Dushelko G., Saeed A.A., Holmes E.C.;
"Sequence variability in the 5' non-coding region of hepatitis C
virus: identification of a new virus type and restrictions on sequence diversity.";
J. Gen. Virol. 74:661-668(1993).
EMBL, U94724; AAB51539.1; -; Genomic_RNA.
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Lerat H., Rumin S., Habersetzer F., Berby F., Trabaud M.-A., Trepo C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                         STRAIN=KNG318;
Chub B.V., Shustov A.V., Netesov S.V.;
"Intergenotypic recombinants of Hepatitis C virus found in Sough
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 2; Length 167;
Pred. No. 3.6;
0; Mismatches 1; Indels
                                                                                                        Siberia."; S. S. Subatred (SEP-2004) to the EMBL/GenBank/DDBJ databases. Subatred (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AY764170; AAV35986.1; -; Genomic_RNA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:005198; F:sErnctural molecule activity; IEA. InterPro; IPR002521; HCV_capsid. InterPro; IPR002521; HCV_capsid.
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G0; G0:0019028; C:viral capsid; IEA.

G0; G0:0005198; F:structural molecule activity; IEA.

G0; G0:0005198; F:structural molecule activity; IEA.

InterPro; IPR002521; HCV capsid.

InterPro; IPR012521; HCV core.

Pfam; PF01542; HCV core; 1.

Pfam; PF01542; HCV core; 1.

Viral nucleoprotein.

NON TER 188 188

SEQÜENCE 188 AA; 20597 MW; 22CFA884F136B44A CRC64;
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188 AA; 20597 MW; 22CFA884F136B44A CRC64;
                                                                                                                                                                                                                                                                                         Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
NON TER 167 167
SEQÜENCE 167 AA; 18299 MW; D3296D178CD710FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 25, Last annotation update)
Nucleocapsid protein (Fragment).
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88.9%;
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O09740 9HEPC

O09740;

AC O09740;

DT 01-JUL-1997 (TrEMBLrel. 04, DT 01-JUL-1997 (TrEMBLrel. 04, DT 01-JUL-1997 (TrEMBLrel. 25, DE Nucleocapsid protein (Fragme OC Hepacitis C virus.

OX Hepacitis C virus.

OX NUTURES; SERNA positive-stra OC Hepacitus C virus.

OX NCBI_TaxID=11103;

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RA Lochauspe G.; Haberset

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RN Dubhelko G.; Saeed A.A.; Holm Norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; identification of a norius; poporosity; il curv.

J. Gen. Virus; identification of a norius; poporosity; il curv.

DR HSSP; QGJTS; il CV. capsid; il nerpro; IPRO05221; HCV capsid; in the PTD NON TER 188 HS SQUENCE 188 AA; 20557 MW SEQUENCE 188 AA; 20557 MM
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R. EMBL, AV26599; AAR34665.1; -; Genomic_RNA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
R. InterPro; IPR002521; HCV_capsid.
R. InterPro; IPR002521; HCV_capsid.
R. Pfam; PF01543; HCV_capsid; 1.
R. Pfam; PF01543; HCV_capsid; 1.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Core protein (Fragment).
Hepatitis C virus.
Viruses, SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBI_TaxID=11103;
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Hepacivirus.
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88.9%; Pred. No. 3;
tive 0; Mismatches 1; Indels
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137 AA; 15022 MW; A8F6C45366AA0B6E CRC64;
                                                                                                                                                                                                                                                                           137 AA; 14962 MW; 6BDB826D178C5F58 CRC64;
J. Gen. virol. 84:2333-2341(2003).

EMBL, AY256800; AAR3464.1; -; Genomic_RNA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR00252; HCV capsid.

InterPro; IPR00252; HCV capsid.

InterPro; IPR0521; HCV core.

Pfam; PF01543; HCV_core; 1.
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QTILG8 9HEPC PRELIMINARY;
QTILG8;
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QSUBV2;
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Matches 8, Conservative
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STRAIN=DK11;
MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Hepacivirus.
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Pred. No. 4;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB077951; BAC03374.1; -; mRNA.
HSSP; Q8JYS1; 1CWX.
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GO; GO:00019028; C:viral capsid; IEA.
InterPro; IPRO02521; HCV capsid.
InterPro; IPRO02521; HCV core.
Pfam; PF01543; HCV core.
NON TER.
191 191
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   Pred. No. 4;
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MEDLINE=94336721; PubMed=8058787;
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88.98;
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Q68107;
Best Local Similarity 88.9
Matches 8; Conservative
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MEDLINE=22913822; PubMed=14550584; DOI=10.1016/S0168-1702(03)00218-1;
Dansako H., Naganuma A., Nakamura T., Ikeda F., Nozaki A., Kato N.;
"Differential activation of interferon inducible genes by hepatitis C
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NUCLECTIDE SEQUENCE.
NMEDLINE=97052554; PubMed=8897188;
Bernier L., Willems B., Delage G., Murphy D.G.;
"Identification of numerous hepatitis C virus genotypes in Montreal,
                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 6.
Viruses; SeRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBI_TAXID=42182;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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EMBL; AB092963; BAC20465.1; -; Genomic_RNA.

HSSP; QBUYS1; ICWX.

GO; GO.0019028; C:viral capsid; IEA.

GO; GO.0019028; F:structural molecule activity; IEA.

InterPro; IPR002522; HCV_capsid.

InterPro; IPR002521; HCV_core.

Pfam; PF01543; HCV_core.

Pfam; PF01543; HCV_core; 1.

Pfam; PF01543; HCV_core; 1.
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GO; GO:0001918; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
Pfam; PF01543; HCV core; 1.
Pfam; PF01542; HCV core; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                       191 AA
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J. Clin. Microbiol. 34:2815-2818(1996).
EMBL; U33435; AAB40038.1; -; Genomic_RNA
HSSP; Q8JYS1; ICWX.
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           11_9HEPC
Q68411_9HEPC PRELIMINARY;
Q68411;
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QBBESO;
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NCBI_TaxID=11103;
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MEDLINE=94336721; PubMed=8058787;
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068115, 9HEPC
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D 068115, 068115, 01-NOV-1996 (TTEMBLEE) 24, 08115, 01-NOV-1996 (TTEMBLEE) 24, 01-NOV-1996 (TTEMBLEE) 24, 01-NOV-1996 (TTEMBLEE) 24, 02 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 03 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 25, 04 01-NOV-1996 (TTEMBLEE) 25, 04 01-NOV-1996 (TTEMBLEE) 27, 04 01-NOV-1996 (TTEMBLEE) 27, 04 01-NOV-1996 (TTEMBLEE) 27, 04 01-NOV-1996 (TTEMBLEE) 27, 04 01-NOV-1996 (TTEMBLEE) 27, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-1996 (TTEMBLEE) 24, 04 01-NOV-19
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Matches 8; Conservative
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                  STRAIN-DKII;

X MEDLINE-93376778; PubMed=8396266;

Bukh J., Purcell R.H., Miller R.H.;

Bukh J., Purcell R.H., Miller R.H.;

T At least 12 genotypes of hepatitis C virus predicted by sequence

T analysis of the putative El gene of isolates collected worldwide.";

Theorem Matl. Acad. Sci. U.S.A. 90:8234-8238 (1993).

E MBL; U10190; AAA21029.1; -; Genomic_RNA.

R MSSP; O8075051; LCWX.

R GO; GO:0051992; F:structural molecule activity; IEA.

InterPro; IPR002521; HCV_capsid.

R InterPro; IPR002521; HCV_capsid.

R Ffam; PF01543; HCV_core; 1.
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MEDLINE-B3376778; PubMed-8396266;

Bukh J., Purcell R.H., Miller R.H.;

T. "At least 12 genetypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";

Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).

PRBL, VIIO195; AAA21034.1; -; Genomic_RNA.

RSSP; O8JYS1; ICW.

GO; GO:0019028; C:viral capsid, IEA.

RGO; GO:0019028; F:structural molecule activity; IEA.

InterPro; IPR002521; HCV_capsid.

RINE-Pro; IPR002521; HCV_capsid.

RINE-Pro; IPR002521; HCV_capsid.

RINE-Pro; IPR002521; HCV_capsid.

Pfam; PF01543; HCV_core; 1.
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Bukh J., Putrcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Hepacivirus.
NCBI_TaxID=11103;
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Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 191;
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191 AA; 20749 MW; 80A2094CA84C212C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Polyprotein (Fragment).
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
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Q68112;
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Bukh J., Purcell R.H., Miller R.H.;
Bukh J., Purcell R.H., Miller R.H.;
"At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238 (1993).
Brist, U10139; AAA21037.1; -; Genomic_RNA.
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Hepacivirus.
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0; Mismatches 1; Indels
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Pred. No. 4;
0; Mismatches 1; Indels
191 191
191 AA; 20729 MW; 1EAP41AF76C02AF9 CRC64;
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191 AA; 20725 MW; 7A7994DF2F0909C6 CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002521; HCV capsid.
InterPro; IPR02521; HCV core.
Pfam; PR01543; HCV capsid; 1.
Pfam; PF01542; HCV core; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
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MEDDINE=2279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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"At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
BEMBL; U10211; AAA21050.1; -; Genomic_RNA.
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MEDLINE=94336721, PubMed=8058787;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis
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GO; GO:0005198; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002521; HCV capsid.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01542; HCV core; 1.
                                                                                       Last sequence update)
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
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                                          01-NOV-1996 (TrEMBLrel. 01, Cr
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01-JUN-2003 (TrEMBLrel. 24, La
Polyprotein (Fragment).
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01-NOV-1996 (TERBLEEL 01, L6
01-JUN-2003 (TERBLEEL 24, L6
Polyprotein (Fragment).
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DT 01-JUN-2003 (TrEMBLEEL) 21,

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RN WCLEOTIDE SEQUENCE.

RY Proc. Natl. Acad. Sci. U.S.P.

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R. HSBP, Q8JYS1, 1CMX.

R. GO, GO:00159028; C:viral capsid; IEA.

RO; GO:00519028; F:structural molecule activity; IEA.

RICEPPO: IPRO0252; HCV copsid.

RICEPPO: IPRO02521; HCV core.

DR Pfam; PP01542; HCV_core; 1.
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
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MEDLINE-94336721; PubMed=8058787; Buth J., Purcell R.H., Miller R.H.; Sequence analysis of the core gene of 14 hepatitis C virus genotypes:";
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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MEDLINE=94336721; PubMed=8058787;
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DE NAME-C;
CN HEPGALILIS C VITUB.
CN WINSEL TAXID=11103;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX STRANN-T;
RX SEQUENCE analysis of the cc
RT SHEAD STRANN-T;
RY SEQUENCE ANALYS,
RY PROC. Natl. Acad. Sci. U.S.A
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MEDLINE=93376778; PubMed=8396266;
MEDLINE=93376778; PubMed=8396266;
Bukh J., Purcell R.H., Miller R.H.;
Bukh J., Purcell R.H., Miller R.H.;
The least 12 genetypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
REMBL; U10230; AAA21069.1; -; Genomic_RNA.
RSP; Q8JYS1; 1CWX.
GO; GO:0019028; C:viral capsid; IEA.
RO; GO:0019028; C:viral capsid; IEA.
RO; GO:005198; F:structural molecule activity; IEA.
RICEPPO: IRRO02522; HCV capsid.
RICEPPO: IRRO02521; HCV capsid.
RICEPPO: IRRO02521; HCV capsid.
REMBL; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFGM; PFG
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Hepacivirus.
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Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis C virus
                                                                                                          Score 43; DB 2; Length 191;
Pred. No. 4;
0; Mismatches 1; Indels
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                                      191 AA; 20815 MW; 33B563C1AD96E1AE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genotypes.";
Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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nes 8; Conservative (
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Q68147_9HEPC PRELIMINARY;
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MEDLINE=93376778; PubMed=8396266;

A Bukh J., Purcell R.H., Miller R.H.;

"At least 12 genetypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";

Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).

RR BEBL; U10226; AAA21065.1; -; Genomic_RNA.

RHSSP; Q8JYS1; 1CWX.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro: IPR002522; HCV_capsid.

R InterPro: IPR002522; HCV_capsid.

R Pfam; PF01542; HCV_capsid; 1.
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Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Hepacivirus.
NCBI_TaxID=11103;
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Bukh J., Purcell R.H., Miller R.H.;
Bukh J., Purcell R.H., Miller R.H.;
"At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
EMBL, U10229; AAA21068.1; -; Genomic_RNA.
HSSP; Q8JYS1; 1CWX.
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191 AA; 20761 MW; 882041ED38514CC1 CRC64;
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GO; GO:0005198; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
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Last annotation update)
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88.9%; Pred. No. 4;
7ative 0; Mismatches 1
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MEDLINE=94336721; PubMed=8058787;
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Mat least 12 genotypes of hepatitis C virus predicted by sequence of the putative El gene of isolates collected worldwide.";

Mat least 12 genotypes of hepatitis C virus predicted by sequence of the putative El gene of isolates collected worldwide.";

MEDLI AAA21070.1; -; Genomic_RNA.

MEDLI S41357; S41357;

MESP; QG1051928; F:structural molecule activity; IEA.

MEDLI PRO05221; HCV core.

MINEAPRO; IPRO05221; HCV core.

METALIS PELS43; HCV core; 1.
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MEDLINE=22279243; PubMed=1317578;
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"Sequence analysis of the core gene of 14 hepatitis C virus
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191 AA; 20759 MW; 96F08C445F98E1B2 CRC64;
                                       Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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MEDLINE=94336721; PubMed=8058787;
Q68148;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-UNW-2003 (TrEMBLrel. 24,
Polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, Polyprotein (Fragment).
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QG8150 9HEPC PRELIMINARY;
Q68150;
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Best Local Similarity 88.9,
Loca 8, Conservative
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                                                                                                          Hepatitis C virus.
                                                                                                                                                                 NCBI_TaxID=11103;
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                                                                                                                                                                                                                          STRAIN=US10;
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NUCLEOTIDE SEQUENCE.
STRAIN=US1;
MEDILINE=92279243; PubMed=1317578;
MEDILINE=92279243; PubMed=1317578;
MEDILINE=92279243; PubMed=1317578;
MEDILINE=9227943; PubMed=1317578;
Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
Bequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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MEDIAINE=93376778; PubMed=8396266;
Bukh J., Purcell R.H., Miller R.H.;
Hat least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. U.S.A. 90.8234-8238 (1993).
ENBL; U10333; AAA21072.1; -; Genomic_RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Bukh J., Purcell R.H., Miller R.H.;
Sequence analysis of the core gene of 14 hepatitis C virus
genotypes."; Acad. Sci. U.S.A. 91:8239-8243(1994).
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MEDLINE=94336721; PubMed=8058787;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis C virus
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR02522; HCV_core.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
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Last annotation update)
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88.9%; Pred. No. 4;
tive 0; Mismatches
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MEDLINE=93376778; PubMed=8396266;
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Q68109;
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01-OCT-2003 (TrEMBLrel
Polyprotein (Fragment)
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NUCLEOTIDE SEQUENCE.
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MEDLINE=95023999; PubMed=7524083;
Stuyver L., van Arnhem W., Wyseur A., Hernandez F., Delaporte E.,
Maertens G.;
                                    Length 192;
                                                                                                                 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                    Score 43; DB 2;
Pred. No. 4.1;
0; Mismatches
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Hepatitis C virus.
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NCBI_TaxID=11103;
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STRAIN=CH114 genotype 2c;
STRAIN=CH114 genotype 2c;
MUCLEOTIDE SEQUENCE.
STRAIN=CH114 genotype 2c;
MEDLINE=Sel1817; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
MARTHANNELLINE PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
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                                Bukh J., Purcell R.H., Miller R.H.;
"At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative E1 gene of isolates collected worldwide.";
Proc. Natl. Acad. Sci. US.A. 90:8234-8238(1993).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
Core protein (Fragment).
Hepatitis C virus.
Viruses; scNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBL_TAXID=11103;
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191 AA; 20770 MW; D0D9700694886D87 CRC64;
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20289 MW; 01750300ADDE2BE8 CRC64;
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88.9%; Pred. No. 4;
iive 0; Mismatches
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Virus Res. 38:137-157(1995).

EMBL; L38257; AAC42208.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005193; FS:Core:

InterPro; IPR002519; HCV_env.

Ffam; PF01542; HCV_env.

Ffam; PF01539; HCV_env; 1.

Envelope protein; Polyprotein; Transmembrane.
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STRAIN=BE104 genotype 2c;
STRAIN=BE104 genotype 2c;
MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
Maertens G.;
Gaps
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QB1558_01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
(NE92) core protein (Fragment).
(NE92) core protein (Fragment).
(Hepatitis C virus.
Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepacivirus.
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88.9%;

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Best Local Similarity
Matches 8; Conserv
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MEDLINE=93224886; PubMed=8385694;

MEDLINE=93224886; PubMed=8385694;

MEDLINE=93224886; PubMed=8385694;

MEDLINE=93224886; PubMed=8385694;

MEDLINE=93224886; PubMed=8385694;

Moderate ovariability in the 5' non-coding region of hepatitis C

Torins: identification of a new virus type and restrictions on sequence at diversity.";

Torins: identification of a new virus type and restrictions on sequence ovariability in the 5' non-coding region of hepatitis C

Torins: identification of a new virus type and restrictions on sequence at diversity.";

Torins: identification of a new virus type and restrictions on sequence ovariation.

Torins: identification of a new virus type and restricting on sequence at diversity.";

J. Gen. Virol. 74:61-668(1993).

FIRE PROBES 77: AAK54689.1; -; Genomic_RNA.

BR PLSP: QBUYE1; LCW.

GO: GO: 00019028; C: viral capsid; IEA.

BR GO: GO: 00019028; C: viral capsid; IEA.

InterPro: IPR002521; HCV capsid.

BR Fiam; PF01542; HCV capsid; I.

BR Pfam; PF01542; HCV_core; I.
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"Classification of hepatitis C viruses based on phylogenetic analysis of the envelope 1 and nonstructural 5B regions and identification of five additional subtypes.";

Proc. Natl. Acad. Sci. U.S.A. 91:10134-10138 (1994).

EMBL; L29633; AAA65816.1; -; Genomic_RNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

InterPro; IRR02519; HCV_core.

InterPro; IRR02521; HCV_core.

Pfam; PF01542; HCV_core; I.

Pfam; PF01542; HCV_core; I.

Pfam; PF01553; HCV_core; I.

Pfam; PF01553; HCV_core; I.
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MEDLINE=1225509; PubMed=11326031;
MEDLINE=1225509; PubMed=11326031;
Alfonso V., Flichman D., Sookoian S., Mbayed V.A., Campos R.H.;
Phylogenetic characterization of genotype 4 hepatitis C virus isolates from Argentina.";
J. Clin. Microbiol. 39:1989-1992(2001).
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Q91TF6;
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Best Local Similarity 86.2
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Length 195;

DB 2;

91.5%; Score 43;

Query Match

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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
Maertens G.;
"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
EMBL; L38325; AAC42180.1; "MRNA.
HSSP; Q&JYS1; LCWX.
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                      Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Pred. No. 4.9;
                        Indels
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GO; GO:0019028; C:viral capaid; IEA.
GO; GO:0019018; C:viral envelope; IEA.
GO; GO:0019018; F:structural molecule activity; IEA.
InterPro; IPR00252; HCV capaid.
InterPro; IPR00252; HCV capaid.
InterPro; IPR00251; HCV core.
InterPro; IPR002519; HCV env.
Pfam; PF0154; HCV capaid; 1.
Pfam; PF01543; HCV core; 1.
Pfam; PF01543; HCV core; 1.
Pfam; PF01541; HCV core; 1.
Pfam; PF01545; HCV env; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 4.1;
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88.9%;
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Q68692;
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068694;
                      8; Conservative
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                                                                                                     132 DLMGYIPVV 140
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1 DLMGYIPAV 9
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Maertens G.;
"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
"I virus Res. 38:137-157(1995).
"B EMBL; L138327; AAC42182.1; -; mRNA.
"SESP, 0301781; 1CM."

R GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
BR GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
BR GO; GO:0005198; F:structural molecule activity; IEA.
BR GO; GO:0005198; F:structural molecule activity; IEA.
BR InterPro; IPR002521; HCV_core.
BR InterPro; IPR002521; HCV_core.
BR Ffam; PF01543; HCV_core: 1.
BR Ffam; PF01543; HCV_core: 1.
BR Ffam; PF01539; HCV_env; 1.
BR Ffam; PF01539; HCV_env; 1.
BR Ffam; PF01539; HCV_env; 1.
BR Envelope protein; Transmembrane.
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"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays and molecular analysis of untypeable samples.";
Virus Res. 38:137-157(1995).
EMBL; L38320; AAG42175.1; -; mRNA.
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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment)
Hepatitis C virus type 2c.
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:eructural molecule activity; IEA.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV env.
Pfam; PF01543; HCV core; 1.
Pfam; PF01543; HCV core; 1.
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Q68687;
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
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NCBI_TaxID=31651;
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THE THE TELLS C. VITUS GENOTYPING by means of 5'-UR/core line probe assays

RT and molecular analysis of untypeable samples.";

REMEL, 1383.22; AAC42177.1; -; mRNA.

REMEL, 1383.22; AAC42177.1; -; mRNA.

ROSP, GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid.

ROSP; GO:0019031; C:viral capsid.

ROSP; GO:0019031; C:viral capsid.

ROSP; GO:0019031; C:viral capsid.

ROSP: REMERPO; IPRO02512; HCV capsid.

RITHERPO; IPRO02519; HCV core.

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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
Maertens G.;
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SEQUENCE D., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,

Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,

Maertens G.;
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                                                                                                                                                                                                                                                                                       01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Core protein (Fragment).
Core protein (Fragment).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Q68696;
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Q68689;
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Matches 8, Conservative
132 DLMGYIPVV 140
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RY ULCECTIDE SEQUENCE.

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Raturver L., Wyseur A., van Arnhem W., Lunel F., Laurente-Puig P.,

Rad Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,

RA Maertens G.;

RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays

RT and molecular analysis of untypeable samples.";

RI mepatitis C virus genotyping by means of 5'-UR/core line probe assays

RY in Res. 38:137-157(1995).

REBL; L38324; AAC42179.1; -; mRNA.

BR HSSP; QG0:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:viral envelope; IEA.

BR GO; GO:0019031; C:viral envelope; IEA.

BR GO; GO:0019031; C:viral envelope; IEA.

BR GO; GO:0015222; HCV_core.

BR InterPro; IPR002522; HCV_core.

BR InterPro; IPR002513; HCV_core.

BR InterPro; IPR002513; HCV_core.

BR InterPro; IPR002513; HCV_core.

BR Ffam; PF01543; HCV_core.

BR Envelope protein; Transmembrane.

Frank Envelope protein; Transmembrane.
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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
Maertens G;
"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
Virus Res. 38:137-157(1995).
EMBL: L38333; AAC42188:1; -; mRNA.
HSSP; Q8JYS1; 1CMX.
                                  01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-NOV-2003 (TIEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hepatitis C virus type 4f.
Viruses; SBRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001903198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
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El protein.
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Best Local Similarity 88.3%,
E.hes 8; Conservative
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Q81262;
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>318
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NCBI_TaxID=31651;
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SEQUENCE
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Hepacivirus.
NCBI_TaxID=11103;
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A Murphy D., Willems B., Deschenes M., Hilzenrat N., Mousseau Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

B RBML, AX4111, AX12079-11.; Genomic RNA.

CO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019021; C:integral to membrane; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0015193; C:viral envelope; IEA.

DR InterPro; IPR002521; HCV_capsid.

DR InterPro; IPR002521; HCV_core.

DR InterPro; IPR002519; HCV_env.

DR Fam; PF01543; HCV_core.

DR Fam; PF01543; HCV_core.

DR Fam; PF01539; HCV_env.

PFam; PF01539; HCV_env.

TRANFLORD FAUTORIES.

KW Envelope protein; Folyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.5%; Score 43; DB 2; Length 317; 88.9%; Pred. No. 6.5;
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and molecular analysis of untypeable samples.";
Virus Res. 38:137-157(1995).
EMBL; 138329; AAC42184.1; -; mRNA.
HSSP; Q8JY21; 1CWX.
GO; GO:0019028; Civiral capsid; IEA.
GO; GO:0019028; Civiral capsid; IEA.
GO; GO:0019011; C:viral envelope; IEA.
GO; GO:0019011; C:viral envelope; IEA.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002519; HCV core.
InterPro; IPR002519; HCV env.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01543; HCV core.
InterPro; IPR002519; HCV env.
Pfam; PF01541; HCV capsid; 1.
Pfam; PF01541; Transmembrane.
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317 AA; 34124 MW; C3AFE2297A4A16EC CRC64;
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317 AA; 34062 MW; 1A3C3B818AD4FFC7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    core protein.
El protein.
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Q68691 9HEPC
ID Q68691_9HEPC PRELIMINARY;
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Gaps

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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV core.
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Q68693;
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Matches 8, Conservative
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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R; Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P., Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J., Maertens G.; "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays and molecular analysis of untypeable samples."; Wirus Res. 38:137-157(1995).
EMBL. L138119; AAQ42164.1; -; mRNA.
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Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                 Length 318;
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318 AA; 34584 MW; 5D3F7649C3C20FIF CRC64;
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GO; GO:0019021; C:viral capadid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:structural molecule activity; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                              91.5%; Score 43; DB 2;
88.9%; Pred. No. 6.5;
ative 0; Mismatches 1
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InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV core.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01543; HCV core; 1.
Pfam; PF01542; HCV core; 1.
Envelope protein; Transmembrane.
InterPro; IPR002521; HCV_core.
InterPro; IPR002519; HCV env.
Pfam; PP01543; HCV_capsid; 1.
Pfam; PP01542; HCV_core; 1.
Pfam; PP01539; HCV_env; 1.
Envelope protein; Transmembrane.
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Q68678;
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>318
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"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
Virus Res. 38:137-157(1995).

"Virus Res. 38:137-157(1995).

"Natura Res. 18:137-157(1995).

"Natura Res. 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 18:137-157(1995).

"Natura Res. 1: 19:137-157(1995).

"Natura Res. 1: 19:137(1995).

"Natura Res. 19:137(1995).

"Natura Res. 19:137(1995).

"Natura Res. 19:137(1995).

"Natura Res. 19:137(1995).

"Natura Res. 19:137(1995).

"Natura Res. 19:1
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MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
Stuyver L., Wyseux A., van Arnhem W., Lunel F., Laurent-Puig P.,
Stuyver L., Wyseux B., Bassit L., Nkengasong J., van Doorn L.-J.,
Maertens G.;
"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
Wirus Res. 38:137-157(1995).
HSSP; Q8JYS1; 1CWX.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            Core protein (Fragment).

Hepatitis C virus type 2c.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 2c.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                          Query Match 91.5%; Score 43; DB 2; Length 319; Best Local Similarity 88.9%; Pred. No. 6.5; Matches 8; Conservative 0; Mismatches 1; Indels
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Envelope protein; Transmembrane.
CHAIN 192 >319 B1 protein.
NON TER 319 319 B1 protein.
SEQÜENCE 319 AA; 34268 MW; 6357221F0F1E5899 CRC64;
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132 DLMGYIPVV 140
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Search completed: January 20, 2006, 22:41:33 Job time : 72 secs

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January 20, 2006, 22:29:13 ; Search time 16 Seconds (without alignments) 54.122 Million cell updates/sec
     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                     283416 seqs, 96216763 residues
                                                                                                                                             Post-processing: Minimum Match 100*
Maximum Match 100*
Listing first 100 summaries
                         OM protein - protein search, using sw model
                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                            US-10-770-117-1
                                                                        1 DLMGYIPAV 9
                                                                                                                                                                    PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
                                                            Title:
Perfect score:
                                                                                    Scoring table:
                                                                                                                                                                 Database :
                                                                         Sequence:
                                                                                                     Searched:
                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	genome polyprotein						genome polyprotein	genome polyprotein	genome polyprotein		genome polyprotein		genome polyprotein	structural protein	polyprotein - hepa	polyprotein - hepa	ř				genome polyprotein	hypothetical prote	polypeptide - hepa	genome polyprotein					genome polyprotein
SUMMARIES	B ID	2 JQ0883	2 JQ0881	_	1 JQ1303		2 S32740	2 JN0265	2 S21471			2 S12707		2 PC1284	2 A44150		2 JQ1926		2 JQ1584	2 S18032	2 S18031	2 S19875	2 PN0677	2 PC2219	1 A45573	1 GNWVCJ	1 GNWVTC	1 GNWVTW	1 \$18030	1 GNWVC3
	Length DB	874	874					322	369	•	•	•	•	513	513	520	523	550	640	782	782	782	787	876	3010	3010	3010	3010	3010	3011
* Query	Match I	91.5	91.5	91.5	91.5	89.4	89.4	o	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	σ	89.4	ഗ	89.4	89.4	89.4	89.4	89.4	89.4	89.4
	Score	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
Result	No.	1	8	m	4	ហ	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

genome polyprotein genome polyprotein phospho-beta-galac betaine aldehyde d genome polyprotein precorrin-3 methyl hypothetical prote formate dehydrogen DNA topoisomerase topoisomerase topoisomerase topoisomerase topoisomerase ly c topoisomerase IV c genome polyprotein dTDP-4-keto-6-deox	F-phospho-beta-giu 6-phospho-beta-giu beta-giucosidase (phospho-beta-giuco 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu 6-phospho-beta-giu probable propionyl hypoxia-induceble conserved hypothet altergan Mal £2- endopeptidase Clp transglycosylase h rod shape-determin conserved hypothet conserved hypothet conserved hypothet conserved hypothet histidinol dehydro citrate carrier pr	citrate-sodium sym citrate carrier pr citrate transport H+-transporting tw Chaperonin 60 alph hypothetical prote hypothetical prote major single-stran tubulin-folding co ribulose-bisphosph ribulose-bisphosph ribulose-bisphosph ribulose-bisphosph ribulose-bisphosph ribulose-bisphosph hypothetical prote hypothetical prote probable inner-mem hypothetical prote probable inner-mem hypothetical prote beta-fructofuranos TDP-glucose-4,6-de	cobalamin blosynch hypothetical prote GTPase activating hypothetical prote L-serine dehydrata hypothetical prote probable glucosylt coccolysin (EC 3.4 Ea59 protein - pha ABC transporter, A hypothetical prote nucleotide diphosp pullulanase (EC 3.)

GANWACH 1130305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 1720305 173

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genome polyprotein - hepatitis C virus (isolate HC-J6)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructorin NS4s; nonstructural protein NS5secies: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JQ1303 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JQ1303 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JQ1303 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JQ1303, S; Sugiyama, Y; Kurai, K; Iizuka, H; Machida, A; Miyakawa, J; Gen. Virol: 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a harmonic mumber: JQ1303; MUID: 92044440; PMID: 1658196
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A. Residues: 1-303 - OKA-
A. Residues: 1-303 - OKA-
A. Residues: 1-303 - OKA-
A. Cross-references: UNIPROT: P26660; UNIPARC: UPI0000131E25; GB: D00944; NID: G221650; PID
A. Cross-references: UNIPROT: P26660; UNIPARC: UPI0000131E25; GB: D00944; NID: G221650; PID
A. Cross-references: UNIPROT: P26660; UNIPARC: UPI000131E25; GB: D00944; NID: G21650; PID
C. Reywords: ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine proteinase; tran
C. Reywords: ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine proteinase; tran
F. 216-191/Product: capsid protein M #status predicted <PM>
F: 190-733/Product: nonstructural protein NS1 #status predicted <NS1>
F: 34-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F: 1011-1619/Product: hypacivirin #status predicted <NS3>
F: 1312/Region: nucleotide-binding motif B
F: 1320-1323/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 2678-2729 «KAT.»
A, Residues: 2678-2729 «KAT.»
A, Residues: 2678-2729 «KAT.»
A, Residues: 2678-2729 «KAT.»
A, Residues: 2678-2729 «KAT.»
A, Residues: 2678-2729 «KAT.»
A, Cross=references: UNIPARC: UPIO0000F5263, GB:D10562, GB:D90518; NID:g221523; PIDN:BAA C; Superfamily: hepatitis C virus genome polyprotein
C, Reywords: ATP; capsid protein, envelope protein; glycoprotein; hydrolase; nonstructue
F;11-115/Product: capsid protein C #status predicted «CRC.»
F;12-115/Product: monstructural protein NS1 #status predicted «NS1.»
F;330-733/Product: nonstructural protein NS2 #status predicted «NS2.»
F;34-1241/Region: mucleotide-binding motif B
F;1316-1321/Region: mucleotide-binding motif B
F;1316-1321/Region: mucleotide-binding motif B
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Fil867-2017/Product: nonstructural protein NS4b #status predicted <AN5>
Fil818-333/Product: nonstructural protein NS5 #status predicted <AN5>
Fil818-333/Product: nonstructural protein NS5 #status predicted <AN5>
Fil86,209,233,299,305,411,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,
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Matches 8; Conserv
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                                                                                                                                                      Occasion: Use protein - hepatitis C virus (strain J7) (fragments)
N;Contains: NSS protein
N;Contains: NSS protein
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: J2-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0883
R;Okamoto, H.
Submitted to JIPID, January 1991
A;Reference number: JQ0879
A;Reference number: JQ0879
A;Reference number: JQ0883
A;Rocession: JQ0883
A;Rocession: JQ0883
A;Rocession: JQ0883
A;Rocession: J874 coKA-
A;Cross-references: UNIPROT:Q7LZX6; UNIPARC:UPI0000178537
A;Experimental source: strain J7
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: polyprotein
F;510-874/Product: NS5 protein (fragment) #status predicted <NS5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome polyprotein - hepatitis C virus (strain J6) (fragments)
N;Contains: NS5 protein
N;Contains: NS5 protein
C;Species: hepatitis C virus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0881
R;Okamcto, H.
submitted to JIPID, January 1991
A;Reference number: JQ0893
A;Reference number: JQ0881
A;Reference number: JQ0881
A;Residues: 1-874 cons.
A;Residues: 1-874 cons.
A;Residues: 1-874 cons.
A;Coss-references: UNIPROT:Q7LZYS; UNIPARC:UPI0000178538
A;Experimental source: strain J6
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
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N,Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4s; nonstructural protein NS4b; nonstructural protein NS5
C; paccies: hepatitis C virus protein 31-Dec-1992 #text_change 09-Jul-2004
C; Accession: A40250; PQ0397; PQ0559
C; Accession: A40250; PQ0397; PQ0559
Virology 188, 331-341, 1992
A; Title: Full-length sequence of a hepatitis C virus genome having poor homology to repc A; Reference number: A40250; MUID:92230232; PMID:1314459
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F;510-874/Product: NSS protein (fragment) #status predicted <NSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
91.5%; Score 43; DB 2; Length 874;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels
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ALIGNMENTS
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Matches 8; Conservative
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Score 42; DB 2;
Pred. No. 1.3;
0; Mismatches
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Pred. No. 1.1;
0; Mismatches
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Matches 8; Conservative
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Best Local Similarity
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N; Contains: amino end of envelope protein M; carboxyl end of capsid protein C

C; Species: hepatitis C virus

A; Note: host Homo sapiens (man)

C; Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

C; Accession: PSUGA

R; Fuchs, K:; Mutz, M.; Schreier, E.; Zachoval, R.; Deinhardt, F.; Roggendorf, M.

Gane 103, 163-169, 1991

A; Title: Characterization of nucleotide sequences from European hepatitis C virus isolat

A; Reference number: JNU265; MUID:91365241; PMID:1653756

A; Accession: PSUGA

A; Reference number: NNA

A; Residues: 1-178 < FUC>

A; Cross-references: UNIPROT: 081275; UNIPARC: UPI00000F0A6E; GB:M61719; NID:9329757; PIDN:

C; Superfamily: hepatitis C virus genome polyprotein

C; Superfamily: hepatitis C virus genome polyprotein

C; Superfamily: hepatitis C virus genome polyprotein

C; Superfamily: hepatitis C virus genome polyprotein

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C; Superfamily: hepatitis C virus genome polyprotein

C; Superfamily: hepatitis C virus genome polyprotein
F;1620-1866/Product: nonstructural protein NS4a #status predicted <N4A>
F;1667-2017/Product: nonstructural protein NS4b #status predicted <N4B>
F;2018-2037/Product: nonstructural protein NS5 #status predicted <N0S>
F;209,234,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,28
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N; Contains: capsid protein C; envelope protein M
C; Species: hepatitis C virus
C; Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C; Accession: $32740
R; Vassilev, V.B.; Viazov, S.O.; Kotova, E.Y.; Nosikov, V.V.
Submitted to the EMBL Data Library, April 1993
A; Reference number: $32740
A; Reference number: $32740
A; Reference number: $32740
A; Residues: 1-189 *VAS>
A; Residues: 1-189 *VAS>
Cross-references: UNIFROT: Q68873; UNIPARC: UPI0000178544; EMBL: X71407
C; Superfamily: hepatitis C virus genome polyprotein
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                                                                                                                                                                                Score 43; DB 1; Length 3033;
Pred. No. 7;
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Pred. No. 0.65;
0; Mismatches 1; Indels
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Best Local Similarity 88.5
---- 8, Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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A;Molecule type: genomic RNA
A;Residues: 1-369 <MOG>
A;Cross-references: UNIPROT:Q68869; UNIPARC:UPI00000F3A9C; EMBL:X65924; NID:g59466;
C;Superfamily: hepatitis C virus genome polygrotein
C;Superfamily: hepatitis C virus genome polygrotein
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R;Li, J.S.; Vicvitski, L.; Tong, S.P.; Trepo, C.
Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
A;Title: Identification of the third major genotype of hepatitis C virus in France.
A;Reference number: PC2060; MUID:94197744; PMID:8147893
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N;Contains: capsid protein; envelope protein
C;Species: hepatitis C virus
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S21471
R;Mogam, W.T.
R;Mogam, W.T.
R;Mogam, W.T.
R;Mogam, W.T.
R;Mosam,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome polyprotein N2 - hepatitis C virus
N;Contains: envelope protein E1; nonstructural protein E2/NS1
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
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0
DB 2; Length 322
                                                                                                                                                         1; Indels
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genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)
Cispecies: hepatitis C virus
Cispecies: hepatitis C virus
Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
Cipatesion: PC1284
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsud: A;Okamoto, H.; Terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: capsid protein; Core protein; envelope protein; monstructural protein; pol; E/1-191/Product: core protein; envelope protein; nonstructural protein; pol; F/1-191/Product: core protein #status predicted <COR>
F/192-372/Product: envelope protein #status predicted <ENV>
F/193-492/Product: NS1 protein (fragment) #status predicted <NS1>
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C;Superfamily: hepatitis C virus genome polyprotein
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A,Cross-references: UNIPROT:Q9IFE5; UNIPROT:036579; UNIPROT:036610; UNIPROT:Q9ELS8;
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A;Title: Interaction of immune sera with synthetic peptides corresponding to A;Reference number: A44150; MUID:92228749; PMID:1373489
                                                                                                                            genome polyprotein - hepatitis C virus (fragment)
N;Contains: ocre protein; envelope protein, NS1 protein
C;Species: hepatitis C virus
C;Species: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 31-Dec-2004
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C;Species: hepatitis C virus
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 31-Dec-2004
C;Accession: A44150
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A;Status: preliminary; not compared with conceptual translation A;Molecule type: genomic RNA
A;Residues: 1-513 <CHI>
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Pred. No. 1.8;
0; Mismatches
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R;Seelig, R.
submitted to the EMBL Data Library, December 1993
A;Reference number: S41288
A;Accession: S41288
A;Mclecule type: genomic RNA
A;Residues: 1-492 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.3.
8, Conservative
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A; Residues: 1-513 < OKA>
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PC1284
                                                 RESULT 12
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N, Contains: envelope protein E1; nonstructural protein E2/NS1
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Species: hepatitis C virus
C,Accession: PC2060
R;Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.
Bjochem. Biophys. Res Commun. 199, 1474-1481, 1994
A;Tille: Identification of the third major genotype of hepatitis C virus in France.
A;Reference number: PC2060; MUID: 94197744; PMID: 8147893
A;Rolecule type: mRNA
A;Residues: 1-411 < LIJ>
A;Cross-references: UNIPROT: 081489; UNIPARC: UP10000178524
C;Keywords: AFP; capsid protein; envelope protein; protein; prodicted <NPE>F;199-383/Product: envelope protein E2/NS1 #status predicted <NPE>F;198-411/Product: nonstructural protein E2/NS1 #status predicted <NPE>F;196,209,234,305,325/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-411 <LIJ3.
A;Residues: 1-411 <LIJ3.
Cross-references: UNIPROT:Q81813; UNIPARC:UPI00000F900B; GB:L12355; NID:g410169; PIDN:
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F;192-335/Product: envelope protein E1 #status predicted <NPE>
F;196,209,234,305,325/Binding site: carbohydrate (Asn) (covalent) #status predicted
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88.9%; Pred. No. 1.4;
1ive 0; Mismatches 1; Indels
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Pred. No. 1.5;
0; Mismatches 1; Indels
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Best Local Similarity 88.9
Matches 8, Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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Genome polyprotein - hepatitis C virus (strain U.K.) (fragment)
NyContains: core protein C; envelope protein E1; envelope protein E2; nonstructural pr C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1584
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J, Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative co
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
                                                                                                                                                             A; Accession: JH0711
A; Molecule type: genomic RNA
A; Mesidues: 1-550 < LIU>
A; Molecule type: genomic RNA
A; Mesidues: 1-550 < LIU>
A; Molecule type: genomic RNA
A; Residues: 1-550 < LIU>
A; Cross-references: UNIPROT: Q7LZV4; UNIPARC: UPI00001784F8; GB:M74888; GB:M74889
A; Orce: the nucleotide sequence is not complete
A; Note: translation of the nucleotide sequence is not complete
C; Superfamily: hepatitis C virus genome polyprotein
C; Reywords: envelope protein; glycoprotein; mostructural protein; nucleocapsid; polyt
F; 191-380/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status
F; 381-514/Product: envelope protein B2 or nonstructural protein NS5 (fragment) #status
F; 515-550/Product: nonstructural protein NS5 (fragment) #status
F; 515-550/Product: nonstructural protein NS5 (fragment) #status
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A;Residues: 1-640 <KUM>
A;Cross-references: UNIPROT:Q68966; UNIPARC:UPI00000EFF23; GB:X84079; NID:g643119; PID
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C, Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; polyp
F;1-131/Product: core protein C #status predicted <CEC>
F;192-389/Product: envelope protein E1 #status predicted <EE1>
F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted
F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted
F;196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (co
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK4
C;Date: 30-Unn-1992 #sequence_revision 30-Unn-1992 #text_change 09-Jul-2004
C;Accession: S18032
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
Submitted to the EMBL Data Library, September 1991
A;Pescription: Sequence analysis of putative structural regions of Hepatitis C Virus:
A;Reference number: S18029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42, DB 2; Length 550;
Pred. No. 1.9;
0; Mismatches 1; Indels
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Pred. No. 2.3;
0; Mismatches 1; Indels
R;Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G. Gene III, 245-250, 1992.
A;Title: Genomic typing of hepatitis C viruses present i A;Reference number: JH0711; MUID: 92290283; PMID:1318245
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Matches 8; Conservative
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A,Molecule type: genomic RNA
A,Residues: 1-782 <HON>
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                                                                                                                                                                                                                                                                                                                  polyprotein - hepatitis C virus (isolate HCV-KF)
N;Concains: C protein; E1 protein; E2/NS1 protein
C;Specials hepatitis C virus
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 05-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 07-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Date: 07-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
A;Recension: J01925; MUD: 93019030; PMID: 1383400
A;Recension: J01925; MUD: 93019030; PMID: 1383400
A;Recension: J01925
A;Residues: 1-520 *ABE>
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N;Contains: C protein; E1 protein; E2/NS1 protein
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: J01926
C;Accession: J01926
C;Accession: J01926
C;Accession: J01926
A;Title: Genomic characterization and mutation rate of hepatitis C virus isolated from A;Accession: J01926
A;Title: Genomic characterization and mutation rate of hepatitis C virus isolated from A;Accession: J01926
A;Molecule type: mRNA
A;Recidues: 1-523 -ABES
A;Cross-references: UNIDARC:UP10000178525; DDBJ:D10687
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
F;1:191/Product: C protein #status predicted <CRR>F;192-383/Product: E1 protein #status predicted <ERP>F;384-523/Product: E2/NS1 protein #status predicted <ERP>
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N;Contains: envelope protein El; envelope protein E2; nonstructural protein NS1; nonstru
C;Species: hepatitis C virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
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Pred. No. 1.8;
0; Mismatches 1; Indels
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Pred. No. 1.8;
0; Mismatches 1; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Matches 8; Conservative
                                                                                   132 DLMGYIPLV 140
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                                           DLMGYIPAV
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polypeptide - hepatitis C virus (type 5a) (fragments)
N;Contains: core protein; E1 (carboxyl end); E2/NS1 (amino end); NS3 protein; NS4A pro C;Species: hepatitis C virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
S;Stuyver, L: Arnhem, W.V.; Wyseur, A.; Maertens, G.
Biochem. Biophys. Res. Commun. 202, 1308-1314, 1994
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A; Residues: 1-876 <STV:
A; Residues: 1-876 <STV:
A; Experimental source: serum
C; Keywords: glycoprotein
F; 1-191/Product: core #status predicted <COE>
F; 192-247/Product: E] (carboxyl end) #status predicted <ERE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT: Q08244; UNIPARC: UPI00000F6521; GB: L20498; NID: g1381031; PI. C, Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: glycoprotein; nonstructural protein
F;196, 209, 234, 250, 305, 325, 421, 427, 452, 536, 544, 560, 580, 627, 649/Binding site: carbohydra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: hepatitis C virus
Cispecies: hepatitis C virus
Cisaces: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cisacession: PN0677
Richo, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Biochem. Biophys. Res. Commun. 196, 780-788, 1993
A;Tille: Genomic typing of hepatitis C viruses from Korean patients: Implications
A;Reference number: PN0677; MUID:94059104; PMID:8240354
      predicted <MAT4>
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                                                                       Length 782
          F;734-782/Product: nonstructural protein 2 (fragment) #status
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A;Title: Cloning and phylogenetic analysis of the core, A;Reference number: PC2219; MUID:94338342; PMID:7520237 A;Accession: PC2219
                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 787 - hepatitis C virus (fragment)
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Pred. No. 3.1;
0; Mismatches
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Pred. No. 2.8;
0; Mismatches
                                                                   Score 42; DB 2;
Pred. No. 2.8;
0; Mismatches
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P;784-837/Product: NS4A #status predicted <NSA>
P;838-876/Product: NS4B #status predicted <NSB>
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Best Local Similarity 88.9
Matches 8, Conservative
                                                                       Query Match 89.4
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-787 < CHO>
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PC2219
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C. Specials: hepatitis C virus
N. Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C. Specias: hepatitis C virus
A; Variety: isolate JK2
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: 518031
R; Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A; Description: Sequence analysis of putative structural regions of Hepatitis C Virus isc
A; Reference number: Sl8031
A; Molecule type: genomic RNA
A; Reference number: isolate JK2
A; Molecule type: genomic RNA
A; Residues: 1-782 +HON3
A; Residues: 1-782 +HON3
A; Residues: 1-782 +HON3
A; Residues: 1-782 HON3
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: care protein; core protein; envelope protein; glycoprotein; nonstructural
C; Keywords: capsid protein; core protein; envelope protein; matatus predicted <a href="https://dx.doc.no.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.number.n
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
A;Variety: isolate JK3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19875
R;Honda, M.; Kaneko, S.; Massahi, U.; Kobayashi, K.; Murakami, S.
Submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A;Accession: S18029
A;Accession: S18075
A;Molecule type: genomic RNA
A;Residues: 1-782 *HON>
A;Residues: 1-782 *HON>
A;Csperfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; mistatus predicted *MAT1>
F;1-191/Product: core protein #status predicted *MAT1>
F;192-383/Product: envelope protein #status predicted *MAT1>
F;384-733/Product: NS1/E2 protein #status predicted *MAT2>
enome polyprotein - hepatitis C virus (isolate JK3) (fragment)
(Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
(Species: hepatitis C virus
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Pred. No. 2.8;
0; Mismatches
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Pred. No. 2.8;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9.
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A, Note setting, Carlo CTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
A, Residues: 1-3010 cTAKS
C, Superfamily: hepatitis C virus genome polyprotein
C, Reywords: ATP, capsid protein, envelope protein; glycoprotein; hydrolase; nonstructu
C, Reywords: ATP, capsid protein C #status predicted cEPS
F, 2-115/Product: envelope protein M #status predicted cMES>
F, 192-389/Product: nonstructural protein NS1 #status predicted cNS1>
F, 300-729/Product: nonstructural protein NS2 #status predicted cNS2>
F, 1007-1615/Product: hepacivirin #status predicted cNS3>
F, 1007-1615/Product: nonelectide-binding motif A (P-loop)
F, 1312-1317/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruction NS4a; nonstructural protein NS4b; nonstructural protein NS5 (Species: heparitis C virus C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 (Accession: A38465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome polyprotein - hepatitis C virus (strain Talwan)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructorein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Structure and organization of the hepatitis C virus genome isolated from huma A,Reference number: A38465; MUID:91140698; PMID:1847440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fil616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fil863-2013/Forduct: nonstructural protein NS4b #status predicted <NAB>
Fi2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
Fi2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
Fi196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi,
J. Virol. 65, 1105-1113, 1991
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40244
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Pred. No. 11;
0; Mismatches 1; Indels
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Pred. No. 11;
0; Mismatches 1; Indels
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Best Local Similarity 88.9
Matches 8; Conservative
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C; pate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; pate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R; Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimot Proc. Natl. Accession: A39253; MUDD: 91088550; PMID: 2175903
A; Friele: Molecule type: genomic RNA
A; Reference number: A39253; MUDD: 91088550; PMID: 2175903
A; Molecule type: genomic RNA
A; Rato, N.; Ohkoshi, S.; Shimotohno, K.
Proc. Jun. Acad. 65B, 219-223, 1989
A; Friele: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
A; Reference number: PS0086
A; Molecule type: genomic RNA
A; Residues: 2650-2707 < KA2>
A; Cross-references: UNIPRAC:UPI00000F7365
A; Cromment: The cleavage sites of this polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: AFP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein;
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N/Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructura
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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                                                                                                                 genome polyprotein - hepatitis C virus (strain JT)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NG4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                  Species: hepatitis C virus
Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
Accession: A45573
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Pred. No. 11;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.>
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GNWVCH
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Notochains: capsid protein C; ervelope protein M; hepacivirin (EC 3.4.21.98) (monstructu
C; Species. Paparitis C virus
C; Species. Paparitis C virus
C; Species. Paparitis C virus
C; Species. Paparitis C virus
C; Species. Paparitis C virus
C; Species. Paparitis C virus
C; State: 19-18-18-2000 Hesquence revision 19-Nay-2000 #text_change 09-Jul-2004
C; Accession: S18001; S33570; A48332; S18029
C; Accession: S18002 S33570; A48332; S18029
C; Accession: A whole genome of hepatitis C virus cDNA was isolated from a single patic
A; Reference number: S18028
A; Richard, M; Romeko, S; Nassahi, W; Nurakami, S.
A; Reference number: S18028
A; Richard, M; Romeko, S; Nassahi, W; Navakami, S.
A; Reference number: S18028
A; Richard, M; Romeko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Romestription: A whole genome of hepatitis C virus cDNA was isolated from a single patic
A; Reference number: S18028
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Richard, M; Raneko, S; Dindra, M; Kobayashi, K; Murakami, S.
A; Romering and S; S; Dindra, M; Kobayashi, K; Murakami, S.
A; Romering and S; S; Dindra, M; Kobayashi, K; Murakami, S.
A; Romering and S; S; Dindra, M; Kobayashi, K; Murakami, S.
A; Romering and S; S; Dindra, M; Kobayashi, K; Murakami, S; S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Raneko, S; Dindra, M; Ran
                                                                                                                                         A, Molecule type: genomic RNA
A, Rolecule type: genomic RNA
A, Rolecule type: genomic RNA
A, Residues: 1-3010 CCHES
C, Superfamily: hepatitis C virus genome polyprotein
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructura
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase;
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase;
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase;
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase;
F, 116-191/Product: carvelope protein M #status predicted cNSI>
F, 127-189/Product: nonstructural protein NS1 #status predicted cNSI>
F, 130-123/Product: nonstructural protein NS2 #status predicted cNS2>
F, 130-123/Product: nonstructural protein NS4 #status predicted cNAA>
F, 1316-1319/Region: nucleotide-binding motif B
F, 1316-1319/Region: nucleotide-binding motif B
F, 1316-1319/Region: nucleotide-binding motif B
F, 13112-1317/Region: nucleotide-binding motif B
F, 1313-1313/Product: nonstructural protein NS4 #status predicted cNAA>
F, 1863-2013/Product: nonstructural protein NS5 #status predicted cNAB>
F, 196, 209, 233, 234, 250, 305, 325, 417, 423, 430, 448, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 207
R;Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S. Viology 188, 102-113, 1992 A;Fitle: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:11314449
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89.4%; Score 42; DB
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches
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betains aldehyde dehydrogenase homolog T24C20.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13006
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; is submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Accession: T13006
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-503 < CHO>
A;Cross-references: UNIPROT: Q9ST81; UNIPARC: UPI00000A828C; EMBL: AL096856; GSPDB: GN0006:
A;Experimental source: cultivar Columbia; BAC clone T24C20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3
A;Introns: 37/1; 84/3; 111/3; 161/2; 192/2; 233/3; 255/3; 278/1; 303/3; 341/3; 367/3;
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
F;46-314/Domain: aldehyde dehydrogenase homology <ALD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cjaccession: JE0395 May Monthly Kitazawa, H.; Kawai, Y.; Itoh, T.; Kamio, Y. R;Saito, T.; Suzuki, M.; Komno, K.; Kitazawa, H.; Kawai, Y.; Itoh, T.; Kamio, Y. Biosci. Biotechnol. Biochem. 62, 2318-2327, 1998
A;Title: Molecular cloning and sequencing of two phospho-beta-galactosidase I and II A;Reference number: JE0395; MUID:99138205; PMID:9972258
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Lactobacillus gasseri
C.Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MES>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1230-1237/Region: nucleotide-binding motif B (P-loop)
F;1316-1319/Region: DEXH motif F B F;1316-1319/Region: DEXH motif F B F;1863-2013/Product: nonstructural protein NS4 #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4 #status predicted <NAB>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <NS5>
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A;Cross-references: UNIPROT:006532; UNIPARC:UPI00000BABA7; DDBJ:AB003927
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3011;
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Pred. No. 11;
0; Mismatches
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Pred. No. 18;
2; Mismatches
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Pred. No. 17;
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ilarity 75.0%;
Conservative
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Best Local Similarity 88.5
Lagaretive 8; Conservative
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Best Local Similarity 85.7
Lag 6; Conservative
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                                                                                                                       Protein NS45, INDESTRUCTURED PROCEEDIN NS4D; NONSTRUCTURED PROCESSION NS42, NONSTRUCTURED PROCESSION NS42, NONSTRUCTURED PROCESSION NS42, NONSTRUCTURED C. Species: hepatitis C virus
A;Note: host Homos sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A36814, A41546
R;Inchauspe, G.; Zebbedes, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
submitted to GenBank, July 1992
A;Pocession: A36814
A;Accession: A
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A,Accession: 840770
A,Accession: 840770
A,Accession: 840770
A,Accession: 840770
A,Accession: 840770
A,Essidues: 1-3011 cOKA>
A,Cross-references: UNIPROT: 003463; UNIPARC: UPI00000F0182; EMBL: D10749; NID: 9221586; PID R; Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990
A,Title: The S'-terminal sequence of the hepatitis C virus genome.
A,Reference number: PC1284; MUID: 91013116; PMID: 2170712
     genome polyprotein - hepatitis C virus (strain H)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4s; nonstructural protein NS4b; nonstructural protein NS5
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1;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 # #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 # #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
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S: Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
F;2-115/Product: capaid protein C #status predicted <CPC>
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A;Residues: 1-513 <OK2>
A;Cross-references: UNIPARC:UPI00000F4078; GB:D00831; NID:g221511; PIDN:BAA00705.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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88.9%; Pred. No. 11;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 DĽMGÝÍPLV 140
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Neich, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. Science 273, 1058-1073, 1996
A,Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A; Reference number: A64300; MUD:96337999; PMID:8688087
A,Scaession: E64300
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A; Meseule type: DNA
A; Residues: 1-379 eBUJ.
A; Cross-references: UNIPROT:Q60316; UNIPARC:UPI000012A5DE; GB:U67459; GB:L77117; NID:95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 c.LMT>
A;Cross-references: UNIPROT:Q94250; UNIPARC:UP1000012ED34; EMBL:U67957; PIDN:AAB07587.
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                                                                                                                                                                                                                                         Cipecies: Caenorhabditis elegans
Cipacies: Caenorhabditis elegans
Cipacies: Caenorhabditis elegans
Cipaces 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipacession: T29715
Rilatreille, P.; Bradshaw, H.
Submitted to the EMBL Data Library, August 1996
A;Description: The sequence of C. elegans cosmid K02H8.
A;Reference number: 220671
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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C,Superfamily: formate dehydrogenase chain B; ferredoxin 2[4Fe-4S] homology
C,Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                 hypothetical protein K02H8.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain Bristol N2; clone K02H8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 74.5%; Score 35; DB 2;
Local Similarity 75.0%; Pred. No. 25;
les 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: X
A;Introns: 40/3; 83/3; 138/3; 156/3; 231/3
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Best Local Similarity 66.7
Matches 6, Conservative
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    31 DIVGYIPYV 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP: K02H8.1
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R;Bult, C.J.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: H81805
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                                                                                                                                                                                                             Gronde polyprotein - hepatitis C virus (isolate EUH1480)

Nicontains cappsid protein C; envelope protein M, hepacivirin (EC 3.4.21.98) (nonstructus)

Nicontains cappsid protein C; envelope protein M, hepacivirin (EC 3.4.21.98) (nonstructus)

C; Species: hepatitis C virus

C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C; Accession: JC5620

R; Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.

Biochen. Biophys. Res. Commun. 236, 44-49, 1997

A; Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant

A; Residues: 1-3014 < CHA.

A; Residues: 1-3014 < CHA.

A; Accession: JC5620

A; MOlecule type: mRNA

A; Accession: JC5620

A; Molecule type: mRNA

A; Residues: 1-3014 < CHA.

A; Cross-reference: UNIPROT:039928; UNIPARC:UPI0000174A01; GB:Y13184

A; Residues: 1-3014 < CHA.

A; Residues: 1-3014 < CHA.

A; Residues: 1-3014 < CHA.

A; Cross-reference: Genotype 5a, which predominates in South Africa

A; Note: the translation of the nucleotide sequence is not complete in this paper

C; Superfamily: hepatitis C virus genome polyprotein

C; Keywords: ATP; Glycoprotein; hydrolase; nucleotide of CEP.

F; 115-7Product: capsid protein C #status predicted < CPC.

F; 115-191/Product: envelope protein M #status predicted < CPC.

F; 130-239/Product: nonstructural protein NO2 #status predicted < NS2-

F; 131-1007/Product: nonstructural protein NO2 #status predicted < NS2-

F; 131-130/Product: nonstructural protein NO2 #status predicted < NS2-

F; 131-1318/Region: nucleotide-binding motif B

F; 131-1318/Region: nucleotide-binding motif B

F; 131-1318/Region: protein Details of No2 #status predicted < NS2-

F; 131-1318/Region: protein Details of No2 #status predicted < NS2-

F; 131-1318/Region: protein Details of No2 #status predicted < NS2-

F; 131-1318/Region: protein Details of NS2 #status predicted < NS2-

F; 131-1318/Region: protein Details of NS2 #status predicted < NS3-

F; 131-1318/Region: protein Details Details Details Details Details Detail
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Drecorrin-3 methylase (BC 2.1.1.-) - Rhodobacter capsulatus
C.Species: Rhodobacter capsulatus
C.Species: Rhodobacter capsulatus
C.Species: Rhodobacter capsulatus
C.Species: Ra-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C.Accession: T03534
R.Vicek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A.Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A.Reference number: Z14955; MUID:97404404; PMID:9256491
A.Accession: T03534
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: L245 cvLc>
A.Status: L245 cvLc>
A.Status: DNA
A.Status: DNA
A.Status: UNIPROT:068097; UNIPARC:UP100000BD1A3; EMBL:AF010496; NID:93128256;
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A,Map position: 1
C;Superfamily: precorrin-3B C17-methyltransferase
C;Keywords: methyltransferase
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34 DIIGYIPA 41
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nes 6; Conserva
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: G81064
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B.A.; ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Telle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81064
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-767 < TET>
A;Cross-references: UNIPROT:Q9JYF6; UNIPARC:UPI00000C4752; GB:AE002511; GB:AE002098; NIC
A;Genetics:
A;Genetics:
A;Genetics: NMB1605
C;Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Natitle; 404, 502-506, 2000

Natitle; Gomplete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.

A; Reference number: A81775; MUID:2022556; PMID:10761919

A; Recession: H81805

A; Residues: prolliminary

A; Residues: 1-765 cPAR>
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R;Belland, R.J.; Morrison, S.G.; Ison, C.; Huang, W.M.
Mol. Microbiol. 14, 311-380, 1994
A;Title: Neisseria gonorrhoeae acquires mutations in analogous regions of gyrA and parC
A;Reference number: 560779; MUID: 95131758; PMID: 7830580
A;Accession: 560780
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
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A,Cross-references: UNIPROT:P48374; UNIPARC:UPI0000131339; EMBL:U08907; NID:g529409; PID
C,Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly
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C;Species: Neisseria gonorrhoeae
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: S60780
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F;5-243/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4
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                                               Length 768
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RESULT 1 US-10-114-823B-3 | US-10-114-823B-3 | Sequence 3, Application US/10114823B | | Publication No. US2030099663A1 | | General Proceduric No. US2030099663A1 | | General Proceduric No. US2030099663A1 | | General Proceduric No. US2030099663A1 | | APPLICANT: MATTNER, FRANK | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | APPLICANT: BUSCHIE, MICHAEL | | FURRENT APPLICATION NUMBER: US/10/114,823B | | CURRENT FILING DATE: 2000-10-02 | | PRIOR APPLICATION NUMBER: A-1680/99 | | PRIOR PRIOR FILING DATE: 1999-10-01 | | NUMBER OF SEQ ID NOS: 24 | | SEQ ID NO 3 | | LENGTH: 9 | | CENTRALE PRIOR | | SEQ ID NO 3 | | TAPE: PRT | | CENTRAL | | CENTRAL | | CORDANISM: Artificial Sequence | | FRATURE | | FRATURE | | COPHER INFORMATION: Peptide | | US-10-114-823B-3

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APPLICANT: Barzofsky, Jay A.
APPLICANT: Sarobe, Pablo
APPLICANT: Pendeton, C. David
APPLICANT: Pendeton, C. David
APPLICANT: Arichi, Tatsumi
APPLICANT: Arichi, Tatsumi
APPLICANT: Major, Marian B.
TITLE OF INVENTION WODIFIED HCV PEPTIDE VACCINES
FILE REFERENCE: 14014-0347/P
CURRENT APPLICATION NUMBER: US/10/770,117
CURRENT FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 1999-08-21
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                Sequence 3, Application US/11082595

Publication No. US20050163797A1

GENERAL INFORMATION:
APPLICANT: PLEITWANN, JULIA-KRISTINA
APPLICANT: BUSCHLE, MICHAEL
APPLICANT: BUSCHLE, MICHAEL
APPLICANT: BUSCHLE, MICHAEL
APPLICANT: MELLING, JAC.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
TITLE OF INVENTION: UNBER: US/11/082,595
CURRENT PILING DATE: 2005-03-17
PRIOR PILING DATE: 2005-04-01
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 9
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US-11-082-595-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: hepatitis C virus
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Fublication No. US20040047877A1
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELENS, Robert
APPLICANT: DELENS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: URMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNWEBER: US/10/651,165
CURRENT APPLICATION WUMBER: US/08/974,690C
FRICH REFERENCE: 2551-94
CURRENT FILING DATE: 1997-11-19
FRIOR PRILING DATE: 1997-11-19
FRIOR FILING DATE: 1997-11-28
FRIOR PRILING DATE: 1993-11-04
FRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFFWARR: Patentin version 3.1
SEQ ID NO 203
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US-10-770-117-2
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100.0%; Score 47; DB 5; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 3.3;
0; Mismatches 1; Indels
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Publication No. US20040052818A1
GENERAL INFORMATION:
APPLICANT: Heinz, Franz X.
APPLICANT: Heinz, Franz X.
TITLE OF INVENTION: ATTENUATED LIVE VACCINE
FILE REFERENCE: U 014666.0
CURRENT APPLICATION NUMBER: US/10/450,649
CURRENT APPLICATION NUMBER: PCT/AT02/00046;
PRIOR PILING DATE: 2002-05-11
PRIOR APPLICATION NUMBER: A 272/2001 AT
PRIOR APPLICATION NUMBER: A 272/2001 AT
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 191
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 88.9
Matches 8; Conservative
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; APPLICANT: Innogenetics N.V.; TITLE OF INNETION: Core-glycosylated HCV envelope proteins; FILE REFERENCE 135 PCT; CURRENT APPLICATION NUMBER: US/10/128,590; CURRENT FILING DATE: 2002-07-22; NUMBER OF SEQ ID NOS: 98; SOFTWARE: Patentin version 3.1; SEQ ID NO 89; LENGTH: 209
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Pred. No. 3.7;
0; Mismatches 1; Indels
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; LOCATION: (193)..(193)
; OTHER INFORMATION: Xaa is any amino acid
US-10-651-165-203
                                                                                                                                                            NAME/KEY: MISC FEATURE
LOCATION: (37)...(37)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (58)...(58)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (66)...(66)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (95)...(95)
OTHER INFORMATION: Xaa is any amino acid
PEATURE:
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NAME/KEY: MISC FEATURE
LOCATION: (173)...(173)
OTHER INFORMATION: Xaa is any amino acid
LOCATION: (5).7(5)
OTHER INFORMATION: Xaa is any amino acid
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INFORMATION: Xaa is any amino acid
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Best Local Similarity 88.9%;
Matches 8; Conservative
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; ORGANISM: hepatitis C virus
US-10-128-590-89
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; ORGANISM: hepatitis C virus US-10-128-590-95
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### Sequence 90, Application US/10128590

### Sequence 90, Application US/10128590

### Publicantion No. US2033010861A1

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| Publication No. US20030108561A1
| GENERAL INFORMATION:
| APPLICANT: Innogenetics N.V.
| TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
| FILE REPERRICE: 13 PCT | CURRENT APPLICATION NUMBER: US/10/128,590 | CURRENT FILING DATE: 2002-07-22 | NUMBER OF SEQ ID NOS: 98 | SOFTWARE: Patentin version 3.1 | SEQ ID NO 95 | LENGTH: 209
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Pred. No. 3.7;
0; Mismatches 1; Indels
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Publication No. US20030108561A1
GENERAL INFORMATION:
   TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
   FILE REFRENCE: 135 PCT
   CURRENT APPLICATION UNMBER: US/10/128,590
   CURRENT APPLICATION UNMBER: US/10/128,590
   NUMBER OF SEQ ID NOS: 98
   SOFTWARE PATENTING DATE: 2002-07-22
   NUMBER OF SEQ ID NOS: 98
   SEQ ID NO 94
   LENGTH: 209
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Pred. No. 3.7;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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; ORGANISM: hepatitis C virus
US-10-128-590-94
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Matches 8, Conservative
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US-10-128-590-95
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RESULT 11
US-10-128-587A-89
Sequence 89, Application US/10128587A
Publication No. US20030152940A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelogents of INVENTION: proteins
TITLE OF INVENTION: proteins
TITLE OF INVENTION: Droteins
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Sequence 90, Application US/10128587A

Sequence 90, Application US/10128587A

Publication No. US203030152940A1

Publication No. US203030152940A1

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/128,587A

CURRENT FILING DATE: 2002-04-24

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin version 3.1

SEQ ID NO 90

LENGTH: 209
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; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-89
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Pred. No. 3.7;
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                    Length 209;
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3; DB 4;
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Pred. No. 3.7;
                  Score 43; DB 4
Pred. No. 3.7;
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ORGANISM: Artificial Sequence
                       91.5%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
                       Query Match 91.5
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                            15 DLMGYIPVV 23
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                                                                                                                       1 DLMGYIPAV 9
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TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
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COMPUTER: IBM PC compatible
CORFWARE: Microsoft Word 6.0 / ASCII text output
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 09-May-2001
PRIOR APPLICATION NUMBER: 08/836,075
FILING DATE: <Unknown>
APPLICATION NUMBER: BP 94870166.9
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
                                                                                                                                                                                                                                                                                                                                                                                                           Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 318;
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Pred. No. 5.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSES:
STREET: P.O. BOX 4433
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
      PRIOR FILING DATE: 1997-11-19
PRIOR APPLICATION WNGHER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 204
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-851-138-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/09851138;
Publication No. US20020183508A1
GENERAL INFORMATION:
APPLICANT: MARRIENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: TEXAS.
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-204
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US-09-851-138-76
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Publication No. US20030152940A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
TITLE OF INVENTION: Droteins
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TITLE OF INVENTION: D
US-10-128-587A-94

Sequence 94, Application US/10128587A

Publication No. US20030152940A1

GENERAL INFORMATION:
TITLE DF INVENTION: CONstructs and methods for expression of recombinant HCV envelope
TITLE OF INVENTION: proteins
FILE REFERENCE: 134 PCT
CURRENT APPLICATION NUMBER: US/10/128,587A

CURRENT FILING DATE: 2002-04-24

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin version 3.1
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, OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus US-10-128-587A-94
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; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-95
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Publication No. US20040047877A1
GENERAL INFORMATION:
APPLICANT: LEROUX-ROBLS, Geert
APPLICANT: MERTENS, Geert
TITLE OF INVENTION: VINUS
TITLE OF INVENTION: VINUS
TITLE OF INVENTION: VINUS
TITLE OF PLOTON: VINUS
TITLE OF THE REFERENCE: 2551-94
CURRENT PELION DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/08/974,690C
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Pred. No. 3.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.5%; Score 43; DB 4; Length 209; Best Local Similarity 88.9%; Pred. No. 3.7; Matches 9; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 8; Conservative
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US-10-651-165-204
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US-10-128-587A-95
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 94
LENGTH: 209
TYPE: PRT
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TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
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                   STATE: TEXAS

STATE: TEXAS

COUNTRY: USA

ZIP: 77210-4433

COMPUTER: READABLE FORM:

MEDIUM TYPE: Flopy disk

CORPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION NDATA:

APPLICATION NUMBER: US/09/851,138

FILING DATE: 09-May-2001

PRIOR APPLICATION NUMBER: B 94870166.9

FILING DATE: 21 Oct 1994

APPLICATION NUMBER: EP 94870166.9

FILING DATE: 22 Oct 1994

APPLICATION NUMBER: EP 95870076.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 91.5%; Score 43; DB 3; Best Local Similarity 88.9%; Pred. No. 5.7; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-851-138-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application US/09899046 Publication No. US20030008274A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 319 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
                                                                                                                                                                                                                                STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.5%; Score 43; DB 3; Length 319; 88.9%; Pred. No. 5.7; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/836,075
FILING DATE: «Unknown»
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 8 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 1NNS:004
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSES: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
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ADDRESSE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                             RESULT 17
US-09-851-138-18
; Sequence 18, Application US/09851138
; Publication No. US20020183508A1
; Publication No. WERTENS, GERT
; APPLICANT: MAERTENS, GERT
STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44, Application US/09851138 Publication No. US20020183508A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 207
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Best Local Similarity 88.9
Matches 8; Conservative
132 DLMGYIPVV 140
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US-09-851-138-44
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US-10-651-165-202
; Sequence 202, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
                                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
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ORGANISM: hepatitis C virus
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Best Local Similarity 86.>
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US-10-651-165-206
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Publication No. US20030064360A1
GENERAL INFORMATION:

TILE OF INVENTION: New sequences of hepatitis C virus
genotypes for diagnosis, prophylaxis and therapy.
                                                                                                                                                                                                                 TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
NUMBER OF SEQUENCES: 270
NUMBER PROBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ZIP: B-9052

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy Disk

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/873,224

FILING DATE: 05-Jun-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362,455
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CORRESPONDENCE ADDRESS:
STREET: Industriepark Zwijnaarde 7, box
CITY: Ghent
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Pred. No. 5.7;
0; Mismatches
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TELECOMMUTATION INFORMATION:
TELEPHONE: 00 32 9 241 07 19
TELEFAX: 00 32 9 241 07 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
FILING DATE:
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
                                                                                                                                         Sequence 144, Application US/09878281
Publication No. US20030032005A1
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
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Best Local Similarity 88.9
Matches 8; Conservative
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; MOLECULE TYPE: protein
US-09-878-281-144
                         132 DLMGYIPUV 140
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1 DLMGYIPAV 9
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US-09-878-281-144
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US-09-873-224-144
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APPLICANT: DELGYS, ROBERT
APPLICANT: DELGYS, ROBERT
APPLICANT: DELGYS, ROBERT
TITLE OF INVENTION: URUS
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: PCT/RE94/03555
PRIOR PLING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER: PCT/RE94/03555
PRIOR FILING DATE: 1993-11-04
NUMBER: PCT/RE94/03555
SPIOR FILING DATE: 1993-11-04
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Publication No. US20040047877A1
EGBREAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: INMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: URUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION WHRER: US/10/651,165
CURRENT FILING DATE: 2003-09-02
PRIOR FILING DATE: 1997-11-19
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Pred. No. 5.7;
0; Mismatches
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88.9%; Pred. No. 5.7;
tive 0; Mismatches
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (319)...(319)
SOTHER INFORMATION: Xaa is any amino acid
US-10-651-165-202
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US-10-651-165-230

(S-quence 230, Application US/10651165
) Sequence 230, Application US/10651165
) Sequence 230, Application US/2004004781
) GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: BLELEXS, Robert

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: US/08/974,690C
PRIOR PILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 230
LENGTH: 319
LENGTH: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DAT
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
TITLE OF INVENTION: VIRUS
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT FILING DATE: 2003-09-02
PRIOR PILICATION NUMBER: US/08/974,690C
PRIOR PILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-0-28
PRIOR FILING DATE: 1993-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATECTION 3.1
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Pred. No. 5.7;
0; Mismatches
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NAME/KEY: MISC FEATURE
LOCATION: (156)...(157)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (161)..(161)
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
FEATURE:
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LOCATION: (149).
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Best Local Similarity 88.9%;
Matches 8; Conservative
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; ORGANISM: hepatitis C virus
US-10-651-165-228
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NAME/KEY: MISC_FEATURE
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LENGTH: 319
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; Publication No. US2004004787A1
; Sequence 217, Application US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-NOELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VINUS
; TITLE OF INVENTION: VINUS
; TITLE OF INVENTION: VINUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: PCT/8P94/03555
; PRIOR APPLICATION NUMBER: PCT/8P94/03555
; PRIOR APPLICATION NUMBER: PCT/8P94/03555
; PRIOR FILING DATE: 1993-11-04
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
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91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels
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Pred. No. 5.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (319)...(319)

UCHER INFORMATION: Xaa is any amino acid
US-10-651-165-206
                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (131)...(131)
OTHER INFORMATION: Xaa is any amino acid
          PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 206
LENGTH: 319
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Publication No. US20040047877A1
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEXY, ROBERT
APPLICANT: MAERTENS, Geert
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, ORGANISM: hepatitis C virus
US-10-651-165-217
                                                                                                                                                                                                                                                                                                   ORGANISM: hepatitis C virus
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Best Local Similarity 88.5
Matches 8; Conservative
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US-10-651-165-228
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US-10-651-165-217
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Gaps

us-10-770-117-1.rapbm

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Query Match
Best Local Similarity 88.3
Bs. Conservative
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Publication No. US20040047877A1

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, ROBert
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNMUNDOMINANT POTOPES
PRIOR APPLICATION NUMBER: US/08/974,690C
PRIOR PILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-38
SOCTION NO 200
LENGTHANE: PATENT VERSION 3.1
SEQ ID NO 200
LENGTHANE SEQ ID NOS: 286
LENGTHANE SEQ ID NOS: 286
LENGTHANE SEQ ID NOS: 286
LENGTHANE SEQ ID NOS: 286
LENGTHANE SEQ ID NOS: 286
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Pred. No. 5.7;
0; Mismatches
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Pred. No. 8.2;
0; Mismatches
                                                            FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (174)...(174)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: MISC FEATURE

COCATION: (233).

COTHER INFORMATION: Xaa is any amino acid
US-10-651-165-230
                         ON: (171)..(172)
INFORMATION: Xaa is any amino acid
                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (177)..(177)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE LOCATION: (232). (232)
OTHER INFORMATION: Xaa is any amino acid
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Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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MISC FEATURE
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yeluciation US/10226629A

publication No. US20030166504A1

general information No. US20030166504A1

general information No. US20030166504A1

general information

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Morham, Scott

APPLICANT: Mobden, Adrian

FILE REPERENCE: 5006.01

CURRENT APPLICATION NUMBER: US/10/226,629A

CURRENT APPLICATION NUMBER: US 60/314,182

PRIOR APPLICATION NUMBER: US 60/314,182

PRIOR FILING DATE: 2001-08-22

NUMBER OF SEQ ID NOS: 736

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LEMENT: 2940
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APPLICANT: MAERTENS, GEET
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VAUS
FILE REPERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT FILING DATE: 1090-109-02
PRIOR APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-310-31
SEQ ID NOS: 286
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 201
LENGTH 450
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Sequence 54, Application US/08854825
Publication No. US2002115061A1
GENERAL INFORMATION:
APPLICANT: CLEARY, Andreas
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
NUMBER OF SEGUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.5%; Score 43; DB 4; Length 2940; 88.9%; Pred. No. 58; vative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 4; Length 450;
Pred. No. 8.2;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Beet Local Similarity 88.30,
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: hepatitis C virus US-10-651-165-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Hepatitis C virus US-10-226-629A-13
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Gaps
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| Sequence 51, Application US/10128711
| Publication No. US20030099634A1
| Publication No. US20030099634A1
| GENERAL INPORMATION:
| APPLICANT: VITIELLO, Maria A. CHESTNUT, Robert W. SETTE, Alessandro D. CELIS, Esteban GRAY, Howard
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING |
| NUMBER OF SEQUENCES: 153 |
| COMPOSITIONS ADDRESSES: CORRESPONDENCE ADDRESSES: STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: San Francisco CITY: 
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ZIP: 94105-1493

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMFUTER: IBM PC Compatible

COMFUTER: IBM PC COMPATIBLE

COMFUTER: BATERIL PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION NUMBER: US/08/197,484

FILING DATE: 26-Apr-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/935,811

FILING DATE: 29-ABN-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 29-ABN-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 29-ABN-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 29-ABN-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-ABN-1992
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88.9%; Pred. No. 1.7e+06;
tive 0; Mismatches 1; Indels
                                       Indels
   Pred. No. 1.7e+06;
0; Mismatches 1;
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REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
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TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
   Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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88.9%; Pred. No. 1.7e+06;
tive 0; Mismatches 1; Indels
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Sequence 212, Application US/09894018

Patent No. US20020119127A1

GENERAL INPORMATION:

APPLICANT: EPINAUNE, Inc.

APPLICANT: Chestnut, Robert

APPLICANT: Chestnut, Robert

APPLICANT: Livingston, Brian

APPLICANT: Livingston, Brian

APPLICANT: Daker, David

TITLE OF INVENTION: MATODS AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

TITLE OF INVENTION: MINIGENES AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND SYSTEM FOR OPTIMIZING

CURRENT APPLICATION NUMBER: US(0)/9/894,018

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

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PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR APPLICATION NUMBER: US 60/284,221
                                                                                                                              COUNTRY: 10sh

ZIP: 60601

COUNTRY: 10sh

ZIP: 60601

COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,825
FILING DATE:
FLING DATE:
APPLICATION NUMBER: US/08/854,825
FILING DATE:
APPLICATION NUMBER: G1230
REGISTRATION NUMBER: 61230
REGISTRATION NUMBER: 61230
TELEPHONE: (312) 616-500
TELEPHONE: (312) 616-5700
TELEPHONE: (312) 616-5700
TELEX: 25-3533
INPORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
ADDRESSEE: Leydig, Voit & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.4%; Score 42;
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; ORGANISM: Transgenic mouse
US-09-894-018-212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLMGYIPAV 9
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APPLICANT: BUSCHLE, MICHAEL
APPLICANT: MELLING, JACK
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
FILE REFERENCE: SONN:016US
CURRENT INLING DATE: 2002-04-01
FRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 24
SOTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH; 9
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002_0.1
CURRENT APPLICATION NUMBER: US/10/371,525
CURRENT PILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/311,784
PRIOR APPLICATION NUMBER: US 09/311,784
PRIOR APPLICATION NUMBER: US 06/085,751
PRIOR PILING DATE: 1999-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-10-114-823B-20
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                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.4%; Score 42; DB 4; L
88.9%; Pred. No. 1.7e+06;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 255, Application US/10371525; Publication No. US20030203869A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
MATTNER, FRANK
BUSCHLE, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9
Matches 8, Conservative
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US-10-371-069-255
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                                                                                                                                                                                                                                                                                                 FEATURE:
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                                         Sequence 130, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION:
CHESTNUT: VITIELLO, Maria A.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES: 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.4%; Score 42; DB 4; Length 9; 88.9%; Pred. No. 1.7e+06; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-10-128-711-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-114-823B-20
; Sequence 20, Application US/10114823B
; Publication No. US20030099663A1
; GENERAL INFORMATION:
APPLICANT: FLEITMANN, JULIA-KRISTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 130:
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Best Local Similarity 88.9
Matches 8; Conservative
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            RESULT 33
US-10-128-711-130
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; Sequence 255, Application US/10371645
; Publication No. US2000216343A1
; GENERAL INFORMATION:
; APPLICANT: EPINGUNE INC.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Livingston, Brian
; APPLICANT: Livingston, Brian
; APPLICANT: Chamule Inc.
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE OF INVENTION: UNBER: US/10/371,645
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR PELLING DATE: 1998-05-13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 255
                                                               APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Hemanson, Gary
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Lishioka, Glenn Y.
APPLICANT: Lishioka, Glenn Y.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002.10
CURRENT FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR APPLICATION NUMBER: US 60/085,751
FRIOR SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
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89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
US-10-371-645-255
Sequence 255, Application US/10371069
Publication No. US20030216342A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Rothman, James E.
APPLICANT: Rothman, James E.
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461061
CURRENT APPLICATION NUMBER: US/10/367,580
CURRENT PILING DATE: 2001-02-27
FRIOR APPLICATION NUMBER: US 09/794,832
PRIOR FILING DATE: 1996-02-13
PRIOR FILING DATE: 1996-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR FILING DATE: 1995-08-18
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REPERSHORE: 3963-20022.13
CURRENT APPLICATION NUMBER: US 09/078,904
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FRASEQ for Windows Version 3.0
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Indels
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1,
Mismatches
                                                                                                                                                                                                                          NS-10-31-260-255
Sequence 255, Application US/10371260
Publication No. US20030220285A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE Inc.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Lishioka, Glenn Y.
APPLICANT: Lishioka, Glenn Y.
APPLICANT: Epimmune Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-367-580-74
; Sequence 74, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
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RESULT 40

US-10-367-593-74

Sequence 74, Application US/10367593

Publication No. US20040071721A1

GENERAL INFORMATION:
APPLICANT: Rothman, James B.
APPLICANT: Hothman, James B.
APPLICANT: Hothman, Alan
APPLICANT: Hothman, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Mayhew, Mark
ITILE OF INNEMITON: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/46.012
CURRENT APPLICATION NUMBER: US/10/367,593

CURRENT APPLICATION NUMBER: US 09/011,645
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1996-08-18
PRIOR PILING DATE: 1995-08-18
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                                                                                                                                                                                                                                                                                                                                                    Query Match 89.4%; Score 42; DB 4; Length 9; Best Local Similarity 88.9%; Pred. No. 1.7e+06; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                     TYPE: PRT
CORGANISM: Artificial Sequence
CRATURE:
FRATURE:
CHIRR INFORMATION: synthetic peptide
US-10-367-580-74
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 74
LENGTH: 9
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ORGANISM: Artificial Sequence
FEATURE:
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Search completed: January 20, 2006, 22:52:29 Job time : 118 secs

1 DLMGYIPLV 9

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